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Addy2585 Manin act: Addy2585 Manin act: Addy2585 Manin acc. Addy2585 Manin acc. Addy2585 Manin acc. Addy2586			siconda e) 11 updates/sec 12 vesscar 202
25-NOV-1991; 18PR-0001/48S. (CORS) CORT WAR REGISCT. Hirtch F, Heefiner A; HeF21200-19901/1/1. HeF2019 Add4685. HE	Bomo sapiems. W0200030587-A2. 02-WW-2000. 24-W07-1599; 99W0-FR002897.	RESULT 1 DISAMPSIST mandard; protein; 202 AA. DISAMPSIST; DISAMPSIS	25 8044 5 979 217 5 MMILTYO 26 8044 5 979 217 5 MMILTYO 27 8044 5 979 217 5 MMILTYO 28 1024 5 979 217 5 MMILTYO 28 1024 5 979 217 5 MMILTYO 28 1024 5 979 217 7 MMILTYO 28 1024 5 979 217 5 MMILTYO 28 1024 5 MMILTY
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RESULT 2
ADQ39295
Query Match 100.0%; Score 1047; DB 3; Best Local Similarity 100.0%; Pred. No. 3e-89;
      has investion relates to a novel merhod for identifying an individual who has an altered tills for identifying mycardial interection. The method comprises detecting a single muchocide polymorphism (NRF) in which one is the muchocide approximate system on the system of the system of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; SEQ ID NO 958; 145pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymerphism the individual is mucleic acids.
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10-MAR-2003; 2003US-0453135P
30-APR-2003; 2003US-0466412P
23-SEP-2003; 2003US-0504955P
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ADQ39284
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ADQ39284 standard; protein; 202

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MDKVETFLRIVQCRSVBGSCGF

202

ADQ39284;

18-NOV-2004

(first entry)

Human myocardial infarction-associated gene derived protein, SEQ ID 947

Myocardial infarction; detection; single nucleotide polymorphism; SNP cardiant; gene therapy; human.

202020 RRR R

(APPL-) APPLERA CORP

Iakoubova O;

Identifying an individual who has an altered risk for developing

N-PSDB; ADQ38456 WPI; 2004-533949/51 Cargill M, Devlin JJ, 20-DEC-2002; 2002US-0434778P. 10-MAR-2003; 2003US-0453135P. 30-APR-2003; 2003US-0466412P. 23-SEP-2003; 2003US-0504955P.

22-DEC-2003; 2003WO-US040978 15-JUL-2004 Homo sapiens

WO2004058052-A2

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Best Local Similarity
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181
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MDKVETFLRIVQCRSVEGSCGF 202
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Pred. No. 8.6e-89;
0; Mismatches 1;
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AAR60516
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Best Local
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                                                    Homo sapiens
                                                                                        Serine protease; Factor-Xa; recognition site; fusion protein cleavage protein folding; growth hormone; sometocropin; primer; polymerase chain reaction; amplification;
                                                                                                                                                                                                                   Human somatotropin
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22-MAR-1995
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Pred. No. 8.6e-89;
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Best Local
                                                                                  Growth homome 1; GHI, ostenpathic, game therapy; procein therapy; dishese; obsetly, infection, extended, injection, settlement, settlement, water recently metabolic syntoms, mod disorder; step disorder; crowth homome dysfunction; familial growth homome distinction; metabolic syntoms; short stature; pituitary storage defect; human; matan; macHn;
                       Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                         12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU11731 standard; protein; 217 AA
                                                                                                                                                                                                                                                                                                                                                                                                    AAU11731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Refolding of polypeptide molecules - using a cyclic process involving denaturing and renaturing conditions to produce a correctly folded prod
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                                                                                                                                                                                                                                                                        hormone 1 gene (GH1), S69L mutant
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93DK-00000139
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Pred. No. 1.4e-87;
0; Mismatches (
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The imposition described a method of detecting variation is growth bormone (CHI), and beserfore and objection of the method as comprises comparing the mulectide asqueeze of this growth bormone translation. It is easily declarated that the comparing the mulectide asqueeze of this growth to identify the mulectide asqueeze of this growth is the control of the comparing the mulectide asqueeze of this growth is the control of the comparing variance for the comparing the control of th
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sequence of the human GH1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                            106 SVEANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD
                                                                                                                                                                 61 YIPKEQKYLFLONPQTSLCFSESIPTPSNREETQQXSNLELLRISLLLIQSWLEPVQFLR
                                                                                                                                                                                                                                     58 -----NPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLR
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                                                                                                                                                                                                                                                                                                                                   1 MATGSRTSLLLAFGLLCLPWLQEGSAFPTIPLSRLPDNASLRAHRLHQLAFDTYQEFEEA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
SVFANSLYYGASDSNYYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1029.5; DB 5; Length 217;
pred. No. 1.4e-87;
0; Mismatches 0; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                      165
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181 ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF 217
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RESULT 6
AAU11719
AAU11719 standard; protein; 217 AA
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AAU11719

12-MAR-2002

Growth hormone 1 gene (GH1), major isoform (tirst entry)

Growth hormone 1/ GHz; esteepathic; gene therapy; procein therapy; dahaptes; obsisty; interton interestable; gene therapy; procein returnion; machabile synthesis general discrete; along discrete; along discrete; general discrete

Homo sapiens

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BX8 WO200185993-A2

14-MAY-2001; 2001WO-GB002126. 15-NOV-2001.

12-MAY-2000; 2000GB-00011459. 14-JUL-2000; 2000EP-00306004.

(UYWA-) UNIV WALES COLLEGE OF MEDICINE.

Cooper DN. Procter AM, Gregory J, Millar DS;

WPI; 2002-089798/12. AS18887

Detecting growth hormone variants (GH1), useful in screening patients for growth hormone irregularities, comprises comparing the nuclootide sequence of a GH1 gene from a test sample with thir of a standard sequence of the human GH1.

Disclosure; Fig 6; 95pp; English.

The symptim described a mathod of defecting writation in growth homose CC [GHI] and therefore GH opportunition in an individual. The mathod comprises comparing the melectide sequence of GHI gene describe the comprise of the melectide sequence of GHI gene described comprises the melectide sequence of GHI gene described for the creating sequence of GHI gene described in the comprise of GHI gene described in a settle in accessing spiciants for genetal homose irregularities or producing variant procedure for transition general gener

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166 ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF 202

Sequence 217 AA

A Green and

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Secret Londi Unitarity, 38.3 % Score 1023 5; DB 5; Longity 217, Matches 202; Concertainty 4 Score 1023 5; DB 5; Longity 217, Matches 202; Concertainty 5 Score 202; Concertainty 6 Score 202; Concertainty 7 Score 202; Concertainty 7 Score 202; Concertainty 8 Score 202; Concertainty 8 Score 202; Concertainty 8 Score 202; Concertainty 9 Score 202; Concertainty 8 Score 202; Concertainty 9 Score 202; Concertainty 9 Score 202; Concertainty 9 Score 202; Concertainty 8 Score 202; Concertainty 8 Score 202; Concertainty 8 Score 202; Concertainty 9 Score 202; Concertainty 8 Score 202; Concertain	he inv (GH1) ompris est sas ariatio	rowth	PSI (-PSI	ို့မှို	(YV	14-1	4	15-	õ	M. 6	· sy	E BR 6.0	g	-	≻	> 15					200
	1997; 95pp; English. Lion described a method of detecting variation in grant before GR dysfunction in an individual. The middle the method of GRI deads in the moleculae sequence of GRI deads, in order with a standard human GRI jone asquence, in order with a standard human GRI jone asquence, in order (GRI variant). The method is uneful in screening pa	(GH1), useful in screening patients morises comparing the nucleotide sample with that of a standard	2-089798/12. AAS1888.	N, Procter MM, Gregory J, Millar	UNIV WALES COLLEGE OF			NOV-2001.		Location/Qualifiers 56 /note= "Wild type Glu substituted by	nthetic.	th hormone 1; dil; osteopathic; gene therapy; procein ti etem; obesity; infection; actomogrally; gipari; procein et ; retention; metabolic syndrome; mood disorders sub et th hormone dyfunction; femilial; growth hormone defice c secure; pituitary storage defect; human; mutant; muto	ene (GH1),	(first	NU11720,	11720 standard; protein; 217	81 ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF	ACHIENTA DE LO CONTROL DE LO CONTROL DE LA C	#I_I_I_I_I_I_I_II_III	MATGSRTSLIJARGLICIEMIQEGGAPPTIPLSRLEDNASLRAHRLHQLAFDTYQEFEBA	Local Similarity 98.38; Score 1029.5; DB 5; Length 217; 106 207; Pred. No. 1.4e.87; Local Conservative 0; Mismatches 0; Indels 15; Gaps

Growth hormon irregularities or preducing wariant processed for treating controlled to the processed for the processed f

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tches' 202; Conservative ery Match Local Similarity 98.3%; Score 1029.5; DB 5; Length 93.1%; Pred. No. 1.4e-87; vative 0; Mismatches 0; Indels 217; 15,

Sequence 217 AA;

58 -----NPQTSLCFSESIPTPSNREETQQXSNLELLRISLLLIQSWLEPVQFLR 105 1 MATGSRTSLLLARGLLCLPMLQBGSAPFIPLSRLPDMSLBARRLHQLAFDTYQBF--- 57 Gaps

AAU11730 standard; protein; 217 AA

AAU11730;

12-MAR-2002 (first entry)

Frowth hormone 1 gene (GH1), K67R mutant

Growth hormon i (di) oursomathir; gene therapy; protein therapy; slaberes obesty; intestion across our dispersion sodium retention; state of agentisms sodium retention; for a constant protein soud dispersion accordance of the constant sound o

ynthetic.

isc-difference Location/Qualifiers
67
/note= "Wild type Lys substituted by Arg"

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5-NOV-2001

14-MAY-2001, 2001WO-GB002126

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The invention described a method of detecting wathint in growth hormone comparing the marketing sequence of GRI Spen obtained from the control of the search of the sequence of GRI Spen obtained from the control of the search of the sequence of GRI Spen obtained from the control of the search of the sequence of GRI Spen obtained from the control of the search of th
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 217 AA;
ABG60633;
                                       ABG60633 standard;
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                                                                                                                                                                                           166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  MATGSRTSLILLAEGLLCLEWIQEGSAEPTIPLSRLEDNASLRAHRLHQLAEDTYQEF---
                                                                                                                                                                                                                                                                                                                                                                                                           MATGSRTSLILARGLICLPWIQEGSAPPTIPLSRLPDNASLRAHRLHQLAPDTYGEFEEA 60
                                                                                                                                                                                           ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF 202
                                                                                                                                                                                                                                                                             SVEANSLYYGASDSNYYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFCTNSHNDD 165
                                                                                                                                                                                                                                                                                                                    YIPKEGRYSFLONDOTSLOPSESIPTPSNREETQQKSNLELLRISHLLIQSWLEDVQFLR
                                                                                                                                                                                                                                                                                                                                                                NPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLR 105
                                                                                                                                                   ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF 217
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2000EP-00306004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                           protein; 217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.1%; Score 1029.5; DB
93.1%; Pred. No. 1.4e-87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1029.5; DB 5; Length 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 57
                                                                                                                                                                                                                                                       180
                                                                                                                                                                                                                                                                                                                                              120
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13-AUG-2002
                       (first entry)
hormone (hGH)
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Transcellular transport; transcytotic transport; paracellular transport; respiratory system disorder; lung canter; tumour, asthma; pathoganic infection; allergy-related disorder; homeoa disorder; patropinedian; homeoa disorder; patropinedian; homeoa disorder; patropinedian; homeoa disorder; patropinedian; Chron's disease; eating disorder; polyimmunoglobulin receptor; pIgR

WO200228408-A2 Homo sapiens

13-NOV-2000; 2000US-0248478P. 14-NOV-2000; 2000US-0248819P. 09-FEB-2001; 2001US-0267601P 02-OCT-2000; (ARIZ-) ARIZEKE PHARM INC 2000US-0237929P

F, Sheridan P. Hawley S, Glynn JM, Chapin

WPI; 2002-416628/44.

complex useful for transporting scrive agent through spithbilal barrier, has biologically active portion and terget cleant directed to ligand that conferm e.g., transproaci proparties to agent specific to ligand. N-PSDB; ABK81192.

The invention described a complex or compound (1) comprising a complex or compound (1) comprising a complex or compound (1) comprising to a client but confirms transcribing, transcribed to the light of comparison to the compound of the co Disclosure; Fig 22; 379pp; English.

Query Match Best Local Matches 61 YIPKEGKYSFLONÞÓTSLÓFSESÍFTÞSNREETOOKSNLELLRÍSLLLÍGSWLEÞVOFLR 120 85 1 MATGSRTSLLLAFGLLCLEWLQBGSAFFTTPLSRLFDNASLRAFRLHQLAFDTYQEFEEA 60 1 MATGSRTSLILAFGLLCLPWLQBGSAFPTIPLSRLEDNASLRAHRLHQLAFDTYQEF--- 57 Similarity SVFANSLVYGASDSNVYDLLKDLEBGIQTLMGKLEDGSPKTGQIFKQTYSKEDTNSHNDD SVEANSLYYGASDSNYYDLLKDLEBGIQTLMGRLEDGSPRTGQIFKQTYSKEDTNSHNDD 165 Conservative 98.34; -NPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEEVQFLR 105 Score 1029.5; DB Pred. No. 1.4e-87 Mismatches Indels 15, Gaps

121

166 ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF 20

Sequence 217 AA;

DB 5; Length 217;

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I (still), and threaters all opinions, the constraint and spread homeone comprises comparing the man location sequence of Childrain is maching comprises the constraint of the Detecting growth hormone variants (GHI), useful in screening patients growth hormone irregulatities, comprises comparing the nucleotide sequence of a GHI game from a test sample with that of a standard sequence of the human GHI. Claim 18; Page; 95pp; English WPI; 2002-089798/12. (UYWA-) UNIV WALES COLLEGE OF MEDICINE 12-MAY-2000; 2000GB-00011459. 14-JUL-2000; 2000EP-00306004. 14-MAY-2001, 2001WO-GB002126. 15-NOV-2001 WO200185993-A2 Misc-difference Growth hormone j. cm; osteopathic; gene therapy; protein therapy; disheres; obsety, infection; ocrossely; gigantism; softim retention; satisfaction; disorder; also discreter; also discreter; also discreter; occurs and control for the control of t Synthetic Homo sapiens short stature; pituitary storage defect; human; mutant; mutein Growth hormone 1 gene (GH1), V136I mutant 12-MAR-2002 AAU11742; AAU11742 invention described a method of detecting variation in growth hormone 181 standard; ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF Procter AM, (first entry) Location/Qualifiers /note= "Wild type Val substituted by Ile" protein; 217 Gregory J, Millar DS ζ 213

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Matches 201;
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                              Sequence 217 AA;
                                                                                                                                                                                                                                                 appear in the specification but has
sequence (AAU11719) given in figure
                                                                                                                                                                                        Local Similarity
             121
                                         106
                                                                    61
SVPANSLVÝGASDŠNÍ YDĽLKOLEBĠÍ QTLMGRLEDGŠPRTGQÍ FKQTYŠKPDTNŠHNDD
                   SVFANSLYYGASDSNYYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD
                                                    YI PKEQKYSPLQNÞÓTSLÓÐSESÍ ÞTÞSNREBTGÓKSNLELLRÍSÍLLLÍÐSNLEÞVOÐLR 120
                                                                          MATGSRTSLLLAPGLLCLEWLOEGSAFFTIPLSRLFDNASLRAHRLHQLAFDTYGEFEEA 60
                                                                                                                           MATGSRTSLLLAPGLICLEWIGEGAPFTIPLSRLPDNASLRAHRLHQLAPDTYQEF---
                                                                                                                                                                       Conservative
                                                                                                                                                                                  98.21,
                                                                                                                                                                               Score 1028.5; DB
Pred. No. 1.7e-87
                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                               been
                                                                                                                                                                                                                                                               created
                                                                                                                                                                                             DB 5;
                                                                                                                                                                                                                                                    from the GH1 wild type
                                                                                                                                                                  Indels
                                                                                                                                                                                          Length
                                                                                                                                                                                          217;
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                                                                                                                                                            Gaps
180
                           165
                                                                               105
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RESULT 11 AAU11726

181 ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF 166 ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVBGSCGF

202

밁 á á B

AAU11726 standard; protein; 217

12-MAR-2002 AAU11726 (first entry)

Growth hormone 1 gene (GH1), I30V mutant.

Growth hormone 1, GH; osteopathic; gene therapy; protein therapy; diabetes; obsety, lifection; acromegaly; gigantism; aedum retent; water remention; metabolic syntheses mod diaorder; sleep diaorder; Growth hormone dysfunction; familial growth hormone deficiency; pituitary storage defect; human; mutant; mutein retention,

Synthetic. Homo sapiens 즟 222

Misc-difference Location/Qualifiers

WO200185993-A2 /note: "Wild type Ile substituted by Val

15-NOV-2001.

12-MAY-2000; 2000GB-00011459 14-JUL-2000; 2000EP-00306004 14-MAY-2001; 2001WO-GB002126

(UYWA-) UNIV WALES COLLEGE OF MEDICINE

WPI; 2002-089798/12. Cooper DN, Procter AM, Gregory J, Millar DS;

Detecting growth hormone variants (GHI), useful in acreening patients for growth hormone irregularities, comprises comparing the nucleotide sequence of a GHI gene from a test sample with that of a standard sequence of the human GHI.

Claim 18; Page; 95pp; English

The invention described a method of detecting variation in growth hormone 1 (GH1), and therefore GH dysfunction in an individual. The method

Gregory J, Millar DS.

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comprises comparing the nucleotide sequence of out gree obtained from the ceal subject with a such time account of control desired for the ceal subject with a such time account of control desired for the subject with the control of the control desired for the control of the c
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ZXTTTX
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                        Growth hormone 1; GMI; osteopathic; game therapy; procest therapy; disheren; obssity; literation; accrossed obstate; apparture retention; settled to accrossed of decoder; place; defended to according to the hormone deficiency decort hormone deficiency about settled to accord to the control of the control 
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                                                                                                                     Misc-difference
                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YIPKEQKYSELQNÞÓTSLÓFSSSÍFÍFSNREETOOKSNLELLRÍSLLLÍOSWLEÞVOFLR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPOTSLCFSESIPTPSNREETQQXSNLELLRISLLLIQSNLEPVQFLR 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALLKNYGLLYCFRKDMDKVBTFLRIVQCRSVEGSCGF 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                      194
                                                                                    /note= "Wild type Lys substituted by Arg"
                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-089798/12
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2000EP-00306004.
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RESULT 13
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                                                                                                                                                                                                                                                                                                                 58 -----NPQTSLCESESIPTPSNREETQQXSNLELLRISLLLIQSWLEPVQFLR 105
                                                                                                                                                                                                                                                                                                                                                                                                               1 WATGSRTSLILLAFGLLCLPWLQEGSAFFTIPLSRLFDNASLRAHRLHQLAFDTYQEF---
                                                                                                                      ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF 202
                                                                                                                                                                                                                                                                     YIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLR
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                                                                         ALLKNYGLLYCFRRDMDKVETFLRIVQCRSVEGSCGF
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120

57

Conservative 98.0%;

Score 1026.5; DB Pred. No. 2.6e-87 Mismatches

DB 5; Length Indels 15,

WO200185993-A2

43

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tiest manage within a man marked con sequence of cold gone obstaind from the virtation (60) revirable. The virtation (80) revirable (10) revi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention described a method of detecting variation in growth hormone (HHI), and therefore GH dysfunction in an individual. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 18; Page; 95pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting growth hormone variants (GHI), useful in screening patients growth hormone irregularities, comprises comparing the nucleotide sequence of a GHI gene from a test sample with that of a standard sequence of the human GHI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000GB-00011459.
2000EP-00306004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Wild type Lys substituted by Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gregory J, Millar DS:
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XXX888888

Claim 18; Page, 95pp; English

Detecting growth hormone variants (GH1), useful in screening patients growth hormone irregularities, comprises comparing the mucleoride sequence of a GH1 gene from a test sample with that of a standard sequence of the human GH1.

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The invention described a subject of describe writing writing speech hormone [031], and therefore of depriments on in an individual the growth hormone come rises comparing the muclectide sequence of coil gene obtained from the worther on [031] writing world with minimal gene sequence, in order to identify growth hormone irregularities or producing variant processes for treating growth hormone irregularities or producing variant processes for treating growth hormone irregularities or producing variant processes for treating growth hormone irregularities or producing variant growth and the growth hormone irregularities or producing variant growth and growth and

RARRARKEKE

WPI, 2002-089798/12. Cooper DN (UYMA-) UNIV WALES COLLEGE OF MEDICINE

Procter AM,

Gregory J, Millar DS

12-MAY-2000; 14-JUL-2000;

2000GB-00011459. 2000EP-00306004.

14-MAY-2001; 2001WO-GB002126 15-NOV-2001 Misc-difference 100 W0200185993-A2

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AAU11735
                                                                                                                                                                                                                                                                                                             Matches
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Best Local (
     AAU11735
                                                                            181
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                                                                                                                                                             106
                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                          201;
                                                                                                                                                                                                                        58
  standard;
                                                                ALLKNYGLLYCFREDMDKVETFLRIVQCRSVEGSCGF
                                                                                 ALLKNYGLLYCFRKOMDKVBTFLRIVQCRSVBGSCGF
                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                    SVFANSLYYGASDSNYYDLLKDLEEGIQTLMGRLEDGSPRTGOIFKQTYSKFDTNSHNDD
                                                                                                                                         SVFANSLYYGASDSNYYDLLKDLEEGIGTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD
                                                                                                                                                                            YIPKEQKYSFLQNÞÓTSLÓÞSESÍ ÞTÞSNREETQQKSNLELLRÍSLLLIQSWLEÞVQFLR
                                                                                                                                                                                                                                    MATGSRTSLLLAPGLLCLPWLQEGSAPPTIPLSRLPDNASLRAHRLHQLAPDTYQEFEEA 60
                                                                                                                                                                                                                                                           MATGSRTSLLLAPGLLCLPWLQEGSAFFTIFLGRLFDNASLRAHRLHQLAFDTYQEF---
                                                                                                                                                                                                                                                                                                       Conservative
protein, 217
                                                                                                                                                                                                      -NPOTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLR
                                                                                                                                                                                                                                                                                                                  97.9%;
                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                             Score 1025.5; DB
Pred. No. 3.3e-87
                                                                                                                                                                                                                                                                                                                              DB 5;
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                           217
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                                                                                                                                                  165
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8 S 당 Ş 밁

Grotch hormone 1 GH1 osteopathic, gone therapy; protein therapy; diabetes; obsetly, infection, extra gigantism; sodium retention, water retention; metabolic syndrome many gigantism; sodium retention (Grotch hormone dystumetrion; feathlial grotch brotch elseptimetrion; shall grotch brotch grotch mutatic mutch); short stature; pituitary storage defect; human; mutatic mutch. Growth hormone 1 gene (GH1), E100K mutant. 12-MAR-2002 (first entry)

¥XXX

Synthetic. Homo sapiens

/note= "Wild type Glu substituted by Lys"

Location/Qualifiers

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crimquiantite and the the early detection and appropriate clinical throughout it disposant or detection method, but the control that the control throughout it disposant or detection method, but the control throughout of the co
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X S S X E F F X E X E X E X E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Growth hormone 1; GRI; osteopathic; game therapy; procesh therapy; disheren; obsatly; lifection; accromended apparties; sodium retention; accromended disection; along disorder; actor retention; sechnolics games and disection; along disorder; according to the second disection; according to the second disection of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Growth hormone 1 gene (GH1), A181V mutant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVFANSLVYGASDSNVYDLLKDLEEGIQTLWGRLEDGSPRTGQIFKQTYSKFDTNSHNDD 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YIPKEQKYSPLQNPQTSLCFSESIPTPSNREETQQKSNLKLLRISLLLIQSWLEPVQFLR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MATGSRTSLLLAFGLLCLEWLQBGSAFPTIPLSRLFDNASLRAHRLHQLAFDTYGEFEEA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MATGSRTSLLLAFGLLCLPWLQEGSAFFTIPLSRLFDNASLRAHRLHQLAFDTYQEF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            /note= "Wild type Ala substituted by Val"
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Pred, No. 3.3e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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14-MAY-2001; 2001WO-GB002126

Job time : 167 secs Search completed: February

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The invention described a method of checking withinted in jorch homomes (1 (1)) amparish the molecular of the individual; he method (1 (1)) amparish the molecular of the period of the send of the se
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peterting growth hormone variants (GHI), useful in screening pattents growth hormone irregularities, comprises comparing the nucleotide sequence of a GHI gene from a test sample with that of a standard sequence of a GHI gene from a test sample with that of a standard sequence of the human GHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYWA-) UNIV WALES COLLEGE OF MEDICINE
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14-JUL-2000; 2000EP-00306004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              appear in the specification but has been created from the GH1 wild type sequence (ANU1719) given in figure 6
                                                        166
                                                                                                                                                                    106
181
                                                                                                                                                                                                                  61 YIPKEQKYSELQNPQTSLCESESIPTPSNREETQKSNLELLRISLLLIQSMLEPVQFLR 120
                                                                                                                                                                                                                                                                                                                                   1 MATGSRTSILLAFGLICLPHLQBGSAFFTIPLSRLEDNASLRAHRLHQLAFDTYQBF---
                                                   ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF 202
                                                                                                           SVFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD 180
                                                                                                                                                               SVEANSLVYGASDSNVYDLLKDLEEGIQTLAGRLEEDGSPRIGQIFKQTYSKFDINSHNDD 165
     VLLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF
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                                                                                                                                                                                                                                                                                -NPOTSLCFSESIPTPSNREETQQXSNLELLRISLLLIQSWLEPVQFLR 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1025.5; DB 5; Length 217;
pred. No. 3.3e-87;
0; Mismatches 1; Indels 15;
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October to the control of the contro	score distribution. Description	icted 1	parameters: 1612378	KVETFLRIVQCRSVEGSCGE 202	ion 5.1.6 OB Compagen Lcd. OB Compagen Lcd. OB Compagen Lcd. OB Compagen Lcd. Solution 174 Seconds (without alignments) Solution 2 Alignments Solution 2

TISSUE=Pituitary; Gu J., Huang Q.-H., Li N.; Xu S.-H., SEQUENCE FROM N.A. (ISOFORM 3). Genomics 4:479-497(1989) [6]

Han Z.-G., Fu G., Chen Z.;

SEGURMEE PROM N.A. PARMED-STATYSO; RECEIVED N. S. SEGURMEE PROM. N. C., Smith D.H., Barrera-Saldana H.A., Galinas R.E., Sashung P.H., Sandras Coult homose locus: mcLectide sequence, biology, and scoutide.;

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Lewis U. Singh R.N., Bonewald L.F.,
Faltered proteolytic cleavage of human
deamidstion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEAMIDATION OF GLN-163 AND ASN-178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid deletions.";
Biochem. Biophys. Res. Commun. 92:511-516(1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lewis U.J., Bonewald L.F., Lewis L.J.,
"The 20,000-dalton variant of human growth hormone:
                                                                                                                          Baumann G.;
Baumann G.;
"Growth hormone heterogeneity in
"Growth hormone heterogeneity in
Horm. Res. 51 Suppl. 1:2-6(1999)
                                          3D-STRUCTURE MODELING.
MEDLINE=88190073; PubMed=3447173;
Cohen F.B., Kuntz I.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION SITES
hormone."
                  "Prediction of the three-dimensional
                                                                                                                                                                                                     MEDLINE=99321812; PubMed=10393484; DOT=10.1159/000053128
                                                                                                                                                                                                                                 REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 256:11645-11650(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                        SER-132 AND
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                                structure of human growth
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                                                                                                                                                                    pituitary and plasma.";
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Matches 201; Query Match Best Local

Conservative

97.9%;

Score Pred.

DB 1,

217 15;

Mismatches No. 8.2e-85;

Indels Length

Gaps

MATGSRTSLILLAFGILCLPWLQEGSAFPTIPLSRLFDWASLRAHRLHQLAFDTYQEF---

MATGSRTSLLLAFGLLCLEWLOBGSAFFTIFLSKLFDNAMLKAHRLHQLAFDTYGEFEEA

60

-NPQTSLCFSESIPTPSNREETQQKSNLBLLRISLLLIQSWLEPVQFLR 105

VARIANT KOWARSKI SYNDROME GLY-138 MEDLINE=97426478; PubMed=9276733; Local Similarity

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Best Local :
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Submitted (APR-2004) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth hormone 1 variant
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05-JUL-2004
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           181
                                                            166
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                                                                                                                                                                                                                                                                                                                                                                                                                                         200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                      ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVBGSCGF 202
                                                                                                   SVFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRTGQIPKQTYSKFDTNSHNDD
                                                                                                                                               SVEANSLYYGASDSNYYDLLXDLEBGIQTLWGRLEDGSPRTGQIFKQTYSKFDTNSHNDD
                                                                                                                                                                                                            YIPKEQKYSFLQNPQTSLCFSBSIPTPSNREETQQKSNLELLRISLLLIQSNLEPVQFLR
                                                                                                                                                                                                                                                                                                                                                                 MATGSRTSLLLAFGLLCLPWLQEGSAFFTIPLSRLFDNASLRAHRLHQLAFDTYQEF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00266; SOMATOTROPIN 1; 1.
PS00338; SOMATOTROPIN 2; 1.
217 AA, 24875 MW; 12DB1B92F63934D8 CRC64;
                                                                                                                                                                                                                                                                                                               MATGSRTSLLLAFGLLCLPWLQEGSAFFTIFLSRLFDNVMLRAHRLHQLAFDTYQEFEBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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(TrEMBLrel. 27,
(TrEMBLrel. 27,
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                                                                                                                                                                                                                                                   -----NPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSHLEPVQPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.5%;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.9e-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1020.5; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Catarrhini;
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217
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ALLKNYGLLYCFRKDMDKVETFLR

ALLKHYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF

SVFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRTGQ: SVFANSLYYGASDSNYYDLLKDLEEGIQTIMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD

I FKQTYSKFDTNSHNDD

165 120 105 60 57 Matches 200; Query Match Best Local Similarity DISULFID

97.3%; 24843 MW;

Score 1018.5; DB | Pred. No. 2.9e-84; By similarity. By similarity. By similarity Somatotropin. FEA295EDE0518674 CRC64;

DB 1;

Mismatches

Indels Length

15; Gaps

1 MATGSRTSLLLLAFGLLCLPWLQEGSAFPTIPLSRLPDNASLRAHRLHQLAPDTYQEF---

MAPGSRTSLLLAFGLLCLPWLQEGSAPPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEA

YIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLR

-NPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLR

SEQUENCE

217 AA; Conservative

Hormone; Pituitary; Signal. SIGNAL 1 26 PRINTS; PR00836; SOMATOTROPIN.
PROSITE; PS00266; SOMATOTROPIN 1;
PROSITE; PS00338; SOMATOTROPIN 2;

Plam; PF00103; Hormone_1;

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HSSP, P01241; 1HWG.
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR001400; Somatotropin.
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P58756;
                                                                                                                                                               EMBL; AF374232; AAL72284.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: OWN-EVEN-
-i- SIMILARITY: Belongs to the somatotropin/prolactin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NPP-2001) to the men/demant/pond database. It major - - - mention is an important to be in growth control. It major other themset to merody growth is no minute the liver and differentiation and politeration of myobiates, it has estimates mains end uptake and protest synthesis in muscle and other memory by furnishing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pan troglodytes (chimpanzes).
Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Independent duplication of
Anthropoidean lineages.";
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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growth hormone gene
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ALLKNYGLLYCFRKOMDKVETFLRIVQCRSVEGSCGF

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SVFANSLYZGASDSNYDLLKDLEEGIQTLAGRLEDGSPRTGQIFXQTYSKFDTNSHNDD SVFANSLYYGASDSNYYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD YIPKEQKYSFLQNPQTSLCFSBSIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLR

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REERRER ROCCCOS GERRITAN
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Submitted (APR-2004) to the E
EMBL; AY613432; AAT11509.1;
HSSP; P01241; 1AXI.
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
Growth hormone 1 variant 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1993 (Rei. 27, Created)
01-0CT-1994 (Rei. 30, Last sequence update)
05-ULL-2004 (Rei. 44, Last sequence update)
Someturopin procureor (Growth hormone) (GH)
hormone, Growth hormone 1).
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InterPro; 179001400 Sometorpojin.
Fedam; 1790103; Rormona 11, 11,
1792178; 1790036; 6000007780171,
179003178; 1790036; 1790037780171,
18003178; 1790038; 17900477780171,
18003178; 1790038; 17900477780171,
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GO; GO:0005179; F:hormone activity; IEA.
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Mammalia; Eutheria;
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                                    MEDLINE-94000724; PubMed=8404617; DOI=10.1210/en.133.4.1744; GOLOS T.G.; Durning M., Fisher J.M., Towler P.D.; Golos T.G.; Golos T.G
                                                                                                                                                                                                                                                                                                                          Macaca milatta (Rhesus macaque)
Bukaryota, Metazos, Chordeta, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOMA MACMU
P33093;
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              pregnancy in the
                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               NCBI TaxID=9544
                                                                                                                                                                                                                                                                                            Cercopithecinae; Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQQKSNLELLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MATGSRTSLLLAFGLLCLPWLQEGSAFFTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MATGGRTSLLLAFGLLCLPWLQEGSAFPTIPLSRLFDNASLRAHRLHQLAFDTYQEF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALLKWYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF
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              rhesus monkey placenta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -NPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ., Mendonca B.B.;
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 4.4e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1016.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                       RESULT 6
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Best Local :
Matches 19:
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HSSP; P01241; 1AXI.
                                                                                              01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
Placental growth hormone
                                                                                                                                                                                                                                                014643;
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                                                                 Name=hGH-V;
                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVEANSLYYGASDGNVYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAAGSRTSLLLAFALLCLPWLQEGSAFPTIPLSRLFDNANLRAHRLHQLAFDTYQEFEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MATGSRTSILLAFGLLCLPWLQEGSAFPTIPLSRLFDNASLRAHRIHQLAFDTYQEF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALLKNYGLLYCFRKDMDXIETFLRIVQCRSVEGSCGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVFANSLVYGTSYSDVYDLLKDLEEGIQTLMGRLEDGSSRTGQIFKQTYSKFDTNSHNND
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                                                                                                                                                                                                                                                                                     PRELIMINARY
                                    (Human)
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179
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                                                                                                                                   05, Created)
05, Last sequence update)
26, Last annotation update)
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Score 981.5; Pred. No. 6.

6.6e-81;

DB 1;

Mismatches

15,

Gaps

57

2C5180341EEC46D0

CRC64; Length 217; Indels

PRT;

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217

IQSWLEPVQFLR

180 120

165

105 60

isoform precursor

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Li C. H., Chung D., Lahm H. N., Sichin S. J.

The prisary enterts of modey pituitary growth hormone.';

The prisary enterts of modey pituitary growth control. Its major

1- WMNTION: Palye on important role in growth control. Its major

role in etimulating body growth is to attamlate the liver and

other tissues to accrete pir. It a stamlates but also estimates

differentiation and proliteration synthesis in muscle and other

which seld upwase and process mythesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=86129460; PubMed=3080959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endocrinology 133:1744-1752(1993)
[2]
SEQUENCE OF 27-217.
                                                                                                                                                                       Direct protein sequencing; Hormone; Pituitary;
                                                                                                                                                                                                    PROSITE; PS00266; SOMATOTROPIN_1;
PROSITE; PS00338; SOMATOTROPIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, L16556; AMA18842.1; -.
                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR009079; 4_helix_cytokine
                                                                                                                                                                                                                                                                                                                      nterPro; IPR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the somatotropin/prolactin family
                                                                                                                                                                                                                                                                PR00836; SOMATOTROPIN
By similarity
By similarity
E -> Q (in Ref.
N -> D (in Ref.
                                                                                                                       Somatotropin
           Q (in Ref.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as its content
           22
                                                                                                                                                                                        Signal.
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                               문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 187
                                                                Revol A., Esquivel D., Santiago D., Barrera-Saldana H.;
*Independent duplication of the growth hormone gene in three
Anthropoidean lineages ",
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databasee.
                                                                                                                                                                                                                        SOM2 PANTR
P58757;
28-FEB-2003
28-FEB-2003
                                                                                                                                         Pan troglodyres (Chimpanzee).
Bukaryota; Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammaila; Eutheria; Primates; Catarrhini; Hominide; Pan.
                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last amnotation update)
Growth hormone veriant precursor (GH-V) (Plachbormone) (Growth hormone 2).
                                                                                                                                                                                                                                                                    PANTR
                                                                                                                                                                                Name=GH2;
                                                                                                                EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE, PS00338,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
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PRINTS; PR00836; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; GO:0005576; C:extracellular; IBA.
GO:0005179; F:hormone activity; IEA.
InterPro; IPR003979; 4 helix cyrokine.
InterPro; IPR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF006060; AAB71828.1; -. HSSP; P01241; 1A22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   placenta.";
J. Clin. Endocrinol. Metab. 83:2878-2885(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning of two novel growth hormone transcripts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-bull-term placenta;
TISSUE-bull-term placenta;
MEDLINE-9837377; PubMed-9709963; DOI=10.1210/jc.83.8.2878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia, Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hes 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                            FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It etimulates both the
           differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other
                                                                                                                                      TaxID=9598;
                                                                                                                                                                                                                                                                                                              181
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                                                                                                                                                                                                                                                                                                        MDKVETFLRIVQCRSVEGSCGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          MATGSRTSLLLARGLLCLPWLQEGSARPTIPLSRLFDNASLRAHRLHQLARDTYQERNEQ
                                                                                                                                                                                                                                                                                                                                MDKVETFLRIVQCRSVEGSCGP
                                                                                                                                                                                                                                                                                                                                                      VYRHLKDLEBGIQTLMWRL
                                                                                                                                                                                                                                                                                                                                                                                            TSLCFSESIFTESNRVKTQQKSNLELLRISLLLIQSWLEFVQLLRSVFANSLVYGASDSN
                                                                                                                                                                                                                                                                                                                                                                                                             TSLCFSESIPTESNREETQQXSNLELLRISLLLIQSWLEEPQQFLRSVFANSLVYGASDSN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                    MAAGSRTSLLLAFGLLCLSWLQEGSAFPTIFLSKLFDNAMLKARKLYQLAYDTYQEFNPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202
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                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                               41, Created)
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SOMATOTROPIN_2;
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23128 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.41;
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                                                                                                                                                                                                                                                                                                                                                      EDGSPRIGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1e-78,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potential
                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata, Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38B64D011A9197C6 CRC64;
                                                                                                                                                                                                                                                                                                            202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                     217
                                                                                                                                                                                                                                                                                                                                                  PNQSYSKFDTKSHNDDALLKNYGLLYCFRKD
                                                                                                                                                                                              (Placenta-specific growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB
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Query Match Best Local

Length

217;

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DISULFID
                           SEQUENCE
                                                                                                                                                                                                                                                                                   Glycoprotein,
SIGNAL
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HSSP; P01241; 1A22;
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SPIES-PAPP entry is copyright. It is produced through a callaboration between the Savies institute of institutements and the Bugg consentation was shown produced in the control of the savies of the control of th
                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00266; SOMATOTROPIN 1;
PROSITE; PS00338; SOMATOTROPIN 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0836; SOMATOTROPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: Secreted.
-i- TISSUE SPECIFICITY: Expressed in the placenta.
-i- SIMILARITY: Belongs to the somatotropin/prolactin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fam; PF00103; Hormone
             217 AA;
                                                                                                                                                       Hormone, Placenta, Signal
1 26 By similar
27 217 Growth horr
79 191 By similar
             24990 MW;
                                                                    By similarity.
By similarity.
                                                                                                                                                                                                Growth hormone variant
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1592A429075677DE CRC64;
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Matches
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                                                     121 SVFANSLVYGASDSNVYRHLKDLEBGIQTLMWRLEDGSPRTGQIFNQSYSKFDTKSHNDD
                                                                                                                                                                                                                                       189;
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ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF
                    ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF 202
                                                                          SVEANSLYYGASDSNYYDLLKDLSBGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD 165
                                                                                                                                                                                                 MATGSRTSLLLAFGLLCLPWLQEGSAFPTIPLSRLFDNASLRAHRLHQLAFDTYQEF---
                                                                                                                                                                                                                                                   Similarity
                                                                                                             YILKEQXYSFLQNPQTSLCFSESIFTESNRVKTQQKSNLELLRISLLLIQSWLEPVQLLR
                                                                                                                                        -----NPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEEPVQFLR
                                                                                                                                                                      MAAGSRTSLLLARGLUCLEWLQBGSAFFTTPLSRLFDMAMLRAHRLYQLAYDTYQBFBBA
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                   91.3%,
                                                                                                                                                                                                                                    .
                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                955.5; DB 1;
No. 1.5e-78;
                                                                                                                                                                                                                                             .5e-78
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PRELIMINARY;
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PRT;

2

Q6FH54; Q6FH54; Q5-JUL-2004 05-JUL-2004 GH2 protein. 4 (TrEMBLrel. 27, 4 (TrEMBLrel. 27, 4 (TrEMBLrel. 27, Last sequence update)
Last annotation update) Created

Bukaryota; Metazoa; Mammalia; Eutheria; SEQUENCE FROM N.A. NCBI_TaxID=9606, Homo sapiens (Human) Chordata; Craniata; Vertebrata; Eutele Primates; Catarrhini; Hominidae; Homo.

Euteleostomi,

Malaet A. Bent L. Mcandinya M. Schick M.
Nachert D. Marsag K. Schick B. Shim B. He
Sorn B. 200 D. Hu Y. Labast J. Shim B. He
Bedi. Children and Children and Children
Bedi. Children and Children and Children
GJ (00.005157) E. Dharmen activity; IB.
Interfor; PRODUNTS, Abila Dyrokine. 34 Henze S., Mar W.,

Pfam; PF00103;

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SOM2
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21-JUL-1986 (Rel
28-FEB-2003 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
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PROSITE; PS001266; SOMATOTROPIN 1; 1.
PROSITE; PS0013018; SOMATOTROPIN 2; 1.
PROSITE; PS0013018; SOMATOTROPIN 2; 1.
PROSITE; PS0013018; SOMATOTROPIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelo
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Growth hormone variant precursor (GH-V) (Plac
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFONES 1 AND 2).
MEDLINES-88243769; PubMed=3379057;
Liebhaber S.A.;
Cooke N.E. Ray J. Emery J.G., Liebhaber S.A.;
MYRO distinct species of human growth hormone-v
                                                                                                                                                                                                                                                                                                                       "The human growth hormone gene family; nuclectide sequences show
recent divergence and predict a new polypeptide hormone.";
DNA 1:239-48 (1982).
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=83182010; PubMed=7169009;
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hormone) (Growth hormone 2)
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          SEQUENCE FROM N.A.
TISSUE=Placenta;
                                                                                  Seeburg P.H.
                                                                                               MEDLINE=89307277; PubMed=2744760;
Chen E.Y., Liao Y.C., Smith D.H.,
                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                               Igout A., Scippo M.L., Frankenne F., Hennen G.;
"Cloming and nuclectide sequence of placental hdH-V cDNA.",
Arch. Inc. Physiol. Blochim. 96:63-67(1988).
                                                                                                                                                                                    MEDLINE=89024984;
                                                                                                                                                                                                                                 proteins
                                                                                                                                                                                                                                              human placenta predict the expression of novel growth
                                                                                                                                                                                                                                                                                                                                                          Seeburg P.H.;
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                                                  Genomics
                                                                      The human growth hormone
                                                                                                                                                                                                 SEQUENCE PROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MATGSRTSLLLAFGLLCLPWLQEGSAFFTIPLSRLFDNASLRAHRLHQLAFDTYQEF---
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                                                  4:479-497 (1989)
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                                                                                                                                                                                                                          263:9001-9006(1988)
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                                                                           locus: nucleotide, sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT
                                                                                                 Barrera-Saldana H.A., Gelinas R.E.,
                                                                                                                                                                                                                                                               hormone-variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Placenta-specific growth
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h hormone
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

PROSITE;

PS00266; SOMATOTROPIN_1; 1.

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Commented to the control of the cont
                                                                ENGL; J03756; AAB55547.1; -
ENGL; J03756; AAB55540.1; -
ENGL; M3851; AAA35891.1; -
ENGL; G03071; AAA53552.1; -
ENGL; G020760; AAR20760.1; -
PIR; A28072; STHUV2.
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1. PRINCTION Plays an important role in growth control. Its major

1. PRINCTION Plays an important role in growth to the liver and

other timese to secrete 187-1. It examinates both the

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asino cated upsche and process in pythesis in mascle and other
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Pfam; PF00103; Hormone 1; 1.
PRINTS; PR00836; SOMATOTROPIN
                                                                                                                                                InterPro; IPR009079; 4 helix cytokine
InterPro; IPR001400; Somatotropin
                                                                                                                                                                                                                                                                                                                                                                                 MIM; 139240;
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Nameri, Synonymandrivi,
Nameri, Synonymand
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collins F.S., Wagner L., Shemmen C.M., Sc
                                                                                                                                                                                                                                                                                                                                 activity;
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                 Pfem: PP00103; Hormone 1; 1.
PRINTS; PR00885; SOMATOTROPIN 1; 1.
PROSITE; PS00386; SOMATOTROPIN 1; 1.
PROSITE; PS00338; SOMATOTROPIN 2; 1.
                                                              Hallock N., Bhert L., Mkomdinya M., Schick M., Eise
Manbert D., Mirmaj M., Schitchen N., Dhom B., Mans
Schim B. G. 200 D., HW. V., Lädest J.,
Schim B. G. 200 D., HW. V., Lädest J.,
BERLICESTER SCHIMERT NEW MEMORIANIS MAN
BERLICESTER SCHIMERT IN MANUAL PRODUCTION OF CONTROL
OF CONCOSSITS: CONTROL NEW INS.
MIRCHEST LEWONDYS J., CHALL CYTOKING.
MIRCHEST LEWONDYS J. CHALL CYTOKING.
      SEQUENCE
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Nammalia; Eutheria; Primates;
                                                                                                                                                                                                                                        GH2 protein
                                                                                                                                                                                    NCBI_TaxID=9606,
                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                               Name=GH2;
                                                                                                                                                                                                                                                   05-JUL-2004
                                                                                                                                                                                                                                                                                   Q6FH32;
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DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      166
                                                                                                                                                                                                                                                                                                                                                                                         121
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                                                                                                                                                                                                                                                                                                                                                                                                  106 SVFANSLVYGASDSNVYDLIKDLEEGTQTLWGRLEDGSPRTGQIFKQTYSKFDTNSHNDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187;
                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                            ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF
                                                                                                                                                                                                                                                                                                                                                             ALLKNYGLLYCFRKDMDKVBTFLRIVQCRSVBGSCGF
                                                                                                                                                                                                                                                                                                                                                                                                                          YILKEQKYSFLQNPQTSLCFSSSIPTPSNRVKTQQKSNLBLLRISLLLIQSWLSPVQLLR
                                                                                                                                                                                                                                                                                                                                                                                SVFANSLVÝGASDSNÝYRHLKDLEEGIQTLMWRLEDGSPRTGQIFNQSÝSKFDTKSHNDD
                                                                                                                                                                                                                                                                                                                                                                                                                                             ----NPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLBPVQFLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAAGSRTSLLLAFGLLCLSWLQEGSAFPTIPLSRLFDNAMLRARRLYQLAYDTYQEFEEA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MATGSRTSLILLAFGLLCLPWLQEGSAFPTIPLSRLFDMASLRAHRLHQLAFDTYQEF---
  217
217 AA;
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                                                                                                                                                                                                                                      (Fragment).
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                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                      (TrEMBLrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                            PKKLININARY
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  25010 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191
215
166
217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24999 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.7%;
                                                                                                                                                                                                                                              27,
                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Growth hormone var
By similarity.
By similarity.
N-linked (GlcNAc.
075C0EF63C15AAF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 939.5; DB 1;
Pred. No. 4.3e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDMDKVETFIRIVQCRSVEGSCGF -> VRVAPGIPNPCAP
LASRDWGEKHCCPLFSSQALTQENSPYSSFPLVNPPGLSLQ
                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTId=VAR_014591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VSP 006203.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLEDGSPRTGQIFNQSYSKFDTKSHNDDALLKNYGLLYCFR
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CRC64;
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Guery Match Best Local

Local Similarity

89.7%; 86.2%;

Score 939.5; DB 2; Length Pred. No. 4.3e-77;

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SOMA SAIBB
ID SOMA S
AC P58343
DT 28-FEE
DT 28-FEE
                                                                              RESULT 12
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QSWNEO
ID QS
                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local !
SOMA SAIBB
P58343;
28-FEB-2003
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                            PRIMTS; PRO0836; SOMATÖTROPIN.; 1. PROSITE; PRO0866; SOMATÖTROPIN 2; 1. PROSITE; PRO0338; SOMATÖTROPIN 2; 1. SEQUENCE 217 AA; 24894 MW; 42582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005576; C:extracellular; IEA
GO; GO:0005179; F:hormone activity;
Pfam; PF00103; Hormone 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P01241; 1A22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
NCBI_TaxID=9509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ateles geoffroyi (Black-handed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Growth hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF374234; AAL72286.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                      ALLKHYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF
                                                                                                                                                                        SVPANSLLYGVSDSDVYEYLKDLEEGIQTLMGRLEDGSPQTGEIFRQTYRKFDINSQNND
                                                                                                                                                                                                    SVFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD
                                                                                                                                                                                                                                   YIPKBQKYSFLQNPQTŠLCPŠEŠIPTPASKKĖTQQKSNLELLRISLLLIQSWFEPVQPLR
                                                                                                                                                                                                                                                                                            MAAGSRTSILLAFTILCLPQLQEAGAPPTIPLSRLLDNAMLRAHRLHQLAFDTYQEFSEA
                                                                                                                                                                                                                                                                                                                     MATGSRTSLLLAFGLLCLPWLQEGSAFPTIPLGRLPDNASLRAHRLHQLAFDTYQEF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALLKWYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVFANSLYYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD
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(TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                              STANDARD,
41, Created)
41, Last seq
                                                                                                                                                                                                                                                                -NPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLR
                                                                                                                                                                                                                                                                                                                                                                             86.8%; Score 908.5; DB 2
82.0%; Pred. No. 2.8e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Santiago D., Barrera-Saldana H.;
o the EMBL/GenBank/DDBJ databases
sequence
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Last annotation update)
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                                           PKT;
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Craniata; Vertebrata;
Platyrrhini; Cebidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                            425829FF41EEAAE6 CRC64;
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Atelinae; Ateles.
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ID SOMA_CALJA
                                                                                                                                                                     RESULT 13
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Tapinotic would not growth homen in primates and emergence of the

species specificity of human growth homens respect.

Nol. Biol. Bool. 1884-831/2001 June 18 growth control. Its major

Town in a trainating hody growth is o stimulate the liver and

other tissues to secret Jor. It stimulates both the stimulates

differentiation and proliferation of spoblasses both the stimulates

and no self spirits you, who will sufficient smalls and other

and the stimulates of the stimulates of the stimulates and the stimulates of the stimulates
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Bukaryota Metazoa: (buoduta: Craniata: Vertabyzta; Eutalosetomi;
Mammalis; Bujbsçla: Primatos; Platyrrhini; Cabidas; Cabinas; Saimiri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This Sites Part entry is copyright. It is produced through a collaboration between the Seas Institute of Bioinformation and the Banj counterform to be burgers in the first produced the part of the burgers in the season in the season in the season in the Banjoon and the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21265430; PubMed=11371582;
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PROSITE; PS00338; SOMATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR009079; 4_helix_cytokine
InterPro; IPR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P01241;
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Q9GMB3;
28-FEB-2003 (Rel. 41,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00103; Hormone_1; 1.
PRINTS; PR00836; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR
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SUBCELLULAR LOCATION: Secreted.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRIGQIFKQTYSKFDINSHNDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YIPKEQKYSFLQNPQTSLCFSESIPTPASKKETQQKSNLELLRISLILIQSWFEEVQLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MATGSRTSLLLAFTLLCLPQLKEAGAFPTIPLSRLLDNAMLRAHRLHQLAFDTYQEFBEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MATGERTSLILLAFGLICLEWIQEGSAFPTIPLSRLFDNASLRAHRLHQLAFDTYQEF---
                                                                                                                                                                                                                                                                 ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF
                                                                                                                                                                                                                                                                                                                                   ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF 202
                                                                                                                                                                                                                                                                                                                                                                                               SVFANSLLYGVSDSDVYEYLKDLEEGIQTLMERLEDGSPRTGAIFRQTYSKFDINSQNDD
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                                                                                                   STANDARD;
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      Created)
Last sequence update
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Pred. No. 6.4
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By similarity.
By similarity.
By similarity.
; 9515289992C529F7 CRC64;
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DISULFID

SEQUENCE CHAIN SIGNAL Hormone;

217 AA; Conservative

Local

Similarity

85.5%; Score 895.5; 11; Mismatches

DB 1; Indels Length

Pred. No. 4.2e-73;

Gaps

57

Interpro; IPR003079; 4 helix_cytokine. Interpro; IPR001400; Somatotropin.

PROSITE; PS00366; SOMATOTROPIN_1; 1.
PROSITE; PS00338; SOMATOTROPIN_2; 1. PRINTS; PRODESS; SOMATOTROPIN Pfam; PF00103; Hormone 1; 1. HSSP, P01241; 1A22.

Pituitary,

Signal. 24959 MW;

Somatotropin.
By similarity.
By similarity.

By similarity E102151A12CE6192 CRC64;

Q866U1; Q866U1; 01-JUN-2003 01-JUN-2003 01-MAR-2004

3 (TrEMBLrel. 24, 3 (TrEMBLrel. 24, 4 (TrEMBLrel. 26,

Last sequence update)
Last annotation update)

PRELIMINARY

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166 121 106

61 YIPKBQKYSFLQNPQTSLCFSESIPTPASKKETQQKSNLELLRMSLLLIQSWFEPVQFLR

MAAGSWTSILLAFTLICLFQLREAGAFFTIFLSRILDNAMLRAHRLHQLAFDTYQEFEEA 60 MATGSRTSILLIAFGLICLEWIQEGSAFFTIFLSRLEDNASLRAHRLHQLAFDTYQEF---

-NPOTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLR

SVEANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSERTGQIEKQTYSKEDTNSHNDD

165

180 120

SVFANSLLYGVSDSDVYEYLKDLEBGIQTLMGRLEDGSPRTGEIFMQTYRKFDVNSQNND

58 -----

181

ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF 202

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ANTING OC. Wallis M.;

**Cloting and binesteriastion of a passive growth bormone encoding
gene from the armone of the bornous statement of the second of the
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Bakaryota Metacoa; Chordata; (Teniata; Vertebrata; Esteleostomi;
Mammala; Butheria; Primates; Platyrrhini; Callitrichidas; Callithrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (Rel. 44, Last annotation update) somatotropin precursor (Growth hormone).
                                                                                                                                                use by non-profit institutions as long as its content is in no wall of the statement is not removed. Usage by and for commercial entires requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration in between the Swigs Institute of Buchicomatics and the EMBL custastion in the the Burphen Bioinformatics Institute. There are no restrictions on its the Burphen Bioinformatics Institute. There are no restrictions on its
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EMBL; AJ297563; CAC03481.1; --
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259:13131-13138(1984).

Chen E.Y., Seeburg P.H.,

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REPORT OF STREET
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Best Local Sin
Matches 175;
                        SEQUENCE FROM N.A. (GENE CSG1).

KEDLINE-SSO0145; PubMedsC200192;

SG1by M.J., Barta A., Baxter J.D., Bell G.I., Eberhardt N.L.

*Analytis of a major human bortionic somatonammotropin gene-
for two functional promoter elements.*;
                                                                                                                                                                                                                                                                                                                                                              POPAGA; DC4407,
21-WL-1986 (Rel. OJ. Created)
01-ARR-1988 (Rel. O7, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Chorionic somatomammotropin hormone precursor
                                                                                                                                                                                      Nomo satyens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Duthoria; Primates; Catarrhini; Hominidae; Homo.
INCB_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                          (Lactogen).
Name=CSH1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSH_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            00: 00:005576; C:extracellular; IBA.
00: 00:005179; F:hormone activity; IE.
InterPro; IRR003079; 4 helix cytokine.
InterPro; IRR01400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Revol A., Esquivel D.E., Barr
"The GH-PL locus a hot-point
Submitted (AUG-2002) to the F
EMBL; AY146625; AAN84505.1;
HSSP, P01241, 1A22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITÉ; PS00266; SOMATOTROPIN 1; 1.
PROSITE; PS00338; SOMATOTROPIN 2; 1.
SEQUENCE 217 AA; 25081 MW; C74B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam, PF00103; Hormone 1, 1.
PRINTS; PR00836; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=15246530; DOI=10.1016/j.gene.2004.03.034
Revol De Mendoza A., Esquivel Escobedo D., Marti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diacental lactogen PL.A.
Pan troglodytes (Chimpanzes).
Bakaryota Metazoa; Chordatea; Craniata; Vertebrata; Rutel®okromi,
Mammalia; Eutheria; Primates; Catarnini; Hominidae; Pan.
NPB_TaxID=9598;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALLKNYGLLYCFRKUNDKVETFLRIVQCRSVEGSCGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YILKEQKYSFLQNPQTSLCFSESIFTPSNMEETQQKSNLELLRISLLLIESWLEPVRFLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----NPQTSLCFSESIPTPSNRBETQQKSNLELLRISLLLIQSWLEPVQFLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAAGERTSLILAFALICIEMIQEAGAVQTVPLSRLFDHAMIQAHRAYQLAIDTYQEFEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MATGSRTSLLLAFGLLCLPWIQEGSAFPTIPLSRLPDNASLRAHRLHQLAFDTYQEF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : between human and chimpanzee
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C74B6262DBA93060 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                 Evidence
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20 55 55
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MEDLINE=72016313; PubMed=5286363;
Sherwood L.M., Handwerger S., McLaurin W.D., Lanner
"Amino-acid sequence of human placental lactogen.";
                                                                                             SEQUENCE OF
                                                                                                                                               Arch.
                                                                                                                                                              MEDLINE=73201971; PubMed=4712450;
Li C.H., Dixon J.S., Chung D.;
"Amino acid sequence of human cho
                                                                                                                                                                                                                                                                               "Construction and analysi
somatomammotropin.";
Nature 270:494-499(1977).
                                                                                                                                                                                                                                                                                                                                                    MEDIINE=78071761; PubMed=593368;
Shine J., Seeburg P.H., Martial J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 50-217 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seeburg P.H.;

"The human growth hormone gene family: nucleotide sequences show recent divergence and predict a new polypeptide hormone.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Placenta, and Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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SEQUENCE FROM N.A. (GENE \Lambdand BOLLNE-87161235; PubMed=3030680;
MEDLINE-87161235; PubMed=3030680;
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Seeburg P.H.,
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MEDLINE=89307277; Pubmed=2744760;
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"Two structurally different genes
placental lactogen hormone."
J. Biol. Chem. 258:3787-3793 (1983)
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Barrera-Saldana H.A., Seeburg P.H.,
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                                                                                                                           J.S., Chung D.;
quence of human chorionic somatomammotropin.";
Biophys. 155:95-110(1973).
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PubMed=7169009;

hormone locus: nucleotide sequence, biology, and D.H., Barrera-Saldana H.A., Gelinas R.E.

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Query Match 83.3
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EMBL, K02401, AAA52115, 1.

EMBL, K15994, AAA52116, 1.

EMBL, 103071, AAA5255, 1.

EMBL, 103071, AAA5555, 1.

EMBL, 103071, AAA5962, 1.1

EMBL, 10002717, AAA9677, 1.

EMBL, 10002717, AA49671, 1.

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Nature New Biol. 235:64-64(1972).
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InterPro; IPR0010079; A. baix cyrokine.
InterPro; IPR001400; SomatorTopin.
Plant PP00101; Normone; 1.1.
PRINTS; PR001046; SOMATOTROPIN.
PRINTS; PR00266; SOMATOTROPIN.
PROSITE; P800236; SOMATOTROPIN.2; 1.1.
PROSITE; P800236; SOMATOTROPIN.2; 1.1.
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Genew; HGNC:2441; CSH2.
H-InvDB; HIX0014076; -.
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PIR, C32435; LCHUC.
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217 AA,
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25020 MW; 235B0DC7A713F431 CRC64;
             83.3%; Score 872.5; DB 1; Length 217;
79.3%; Pred. No. 5.2e-71;
Live 11; Mismatches 19; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                      IS -> L (In CSH2).

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Interchain (with C-208 in a dimer).
P -> A (in CSH2; dbSNP:1805274).
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Indels 15; Gaps

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57	MATGSRTSLILAFGLICLPMLQEGSAFFTIPLSRLFDNASLRAHRLHQLAFDTYQEF 57	_	×

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ALIGNMENTS

HORS NIH-MGC http://mgc.nci.nih.gov/. Rational Institutes of Health, Mammalian Gene Collection (Mac)		E Homo sapiens (human)	ON CD513951.1 GI:31445669 RDS EST.	IMAGE:30393581 5', mRNA sequence.	TITION AGENCOURT 14375351 NIH MGC 179 Homo gardene Chun Charles	755 hn may 1
ion (Moor)	huteleostomi, Homo.			ě	EST 06-JUN-2003	

/organism="Homo sapiens"

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41 LeuhrghlaHishrgLeuHisGlnLeuhlapheAspThrTyrGlnGlupheAsnProGln 60 21 LeuGlnGluGlySerAlaPheProThrileProLeuGerArgLeuPheAspAsnAlaSer 40 43 Ansacrackascreecakascreecascreecascrrrassecraceraceraceras MetAlaThrGlySerArgThrSerLeuLeuLeuAlaPheGlyLeuLeuCysLeuProTrp Ę 문 ð

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Tissue Procurement: Dr. Michael Brownstein
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128

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1 MetalaThrGlySerArgThrSerLeuLeuLeuAlaPheGlyLeuLeuCysLeuProTrp

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ORIGIN

REFERENCE AUTHORS TITLE COMMENT

Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Bukaryota, Metazoa, Chordata, G Mammalia, Butheria, Primates, C 1 (bases 1 to 797) NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, SOURCE KEYWORDS VERSION DEFINITION CD107947

ORGANISM

Homo sapiens Homo sapiens (human) CD107947.1 GI:30761121 CD107947 CD107947

Catarraini;

Craniata; Vertebrata; Euteleostomi; Mammalian Gene Collection (MGC)

ACCESSION

CD107947 14016184 NIH MC-179 Homo sapiens CDNA clone TMAGE:30365079 5', mRNA sequence.

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                                                     ATGGAACAAGGTCGAGACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTG
                                                                     MetAsp-LysValGluThrpheLeuArglleValGlnCysArgSerValGluGlySerCy
                                                                                                                 SerHisAsnAspAspAlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAsp
                                                                                                                                                                             GATISGEAGCCCCCGGACTOGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAAC
                                                                                                                                                                                                      AspGlySerProArgThrGlyGlnIlePheLysGlnThrTyrSerLysPheAspThrAsn
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High quality sequence stop: 624.
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        ACTOGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC
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                                                                                                                                                                                                                                                    LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 145
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AGENCOURT 13980152 NIH MGC_179 Homo sapiens CDNA clone
IMAGE:30367958 5', mRNA sequence.
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http://image.llnl.gov
Plate: NDAM429 row: p column: 15
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
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NIH-MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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// lab bedi-MERIOFO.A. (T and TS phage resistances)*
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166 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu 185

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-----AsnProGlnThrSerLeuCysPhe

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ORM Library Argued by: The I.M.G. B. Commortium (LIAM)
MR. Sequencing by: Agencourt Bioncience Composition (LIAM)
Clone distribution: MCC Clone distribution information can
found through the I.M.A.G.E. Consortium/LIAM, at:
http://magg.lih.la.jov.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Daniela S. Gorhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bidg: 31 Rm10A07 Bethesda, MD 20892
                                                                                                                                                                                                                                                                                                                                                                   Plate: NDAM448 row: i column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
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National Institutes of Health, Mammalian
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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IMAGE:30383909 5', mRNA sequence.
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Location/Qualifiers
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(clome_lib=wiff MXC_179*

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                                                                                                                                                                                                      /organism="Homo sapiens
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                         clone=*IMAGE:30383909"
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Query Match:
                             Best Local Similarity:
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                                                                                        Scores:
                                                                                                                                     directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC
                                                                                                                               Library.*
2.71e-112
1024.50
92.63%
92.63%
97.85%
           Length:
Matches:
Conservative:
Mismatches:
Indels:
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Score:

ORIGIN

US-09-856-796B-2 (1-202) x CD251158 (1-800)

Gaps:

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MGE:30368844 5', mRNA sequence
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Enkaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 801)

EST

Homo sapiens CD108743.1 GI:30761917 CD108743

Sapiens

(numan)

Homo

sapiens

CDNA clone

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COMMENT
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ORM Library Fesparation; Invitrogen Comportium (LiML)

ORM Library Fesparation; The I.M.A.G.E. Comportium (LiML)

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Mational Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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AAGGACCTAGAGGAAGCATCCAAACGCTGATGGGGAAGGCTGGAAGATGGCAGCCCCCGG 520
                                                            LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 145
                                                                                                                               AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA 460
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Location/Qualifiers
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Tissue procurement: Dr. Michael Brownstein
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Library."
                                                                                                                               /tissue_type="Pituitary"
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/clome_lb="Null MGC_179"
/clome_lb="Null MGC_179"
/note="Organ: bTain' Vector: pCMV-SPORT6,1; Site_1: EcoRV
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/db_xref="taxon:9606"
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Plate: NDAM473 row: g column:
High quality sequence stop: 701.
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National Institutes of Health, Mammalian
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                                               /Organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                    location/Qualifiers
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86 LeufieuArgIleSerLeufeufeufleGinSerTrpLeuGluProValGinPheLeuArg

TCAGAGTCTATTCCGACACCCTCCAACAGGGAAACACACAGAAATCCAACCTAGAG SerGluSerIleProThrProSerAsnArgGluGluThrGlnGlnLysSerAsnLeuGlu

322 85 262

CTGCTCCGCATCTCCCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu

44 125 382 105 -AsnProGlnThrSerLeuCysPhe

65

143

82

57

143

CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGAAGAAGCC 201 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe-----LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAspAspAlaSer 40 CTTCAAGAGGGCAGTGCCTTCCCCAACCATTCCCCTTATCCAGGCTTTTTGACAACGCTATG

83 21 23

MetAlaThrGlySerArgThrSerLeuLeuLeuPhalaPheGlyLeuLeuCysLeuProTrp

/clone="IMAGE:30394616"

623 186 563

ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC ThrPheLeuArgIleValGinCysArgSerValGluGlySerCysGlyPhe 202 ACTOGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC ThrGlYGlnIlePhcLysGlnThrTyrSerLysPhcAspThrAsnSerHisAsnAspAsp Washelougluglugly11edlmhrlaumetglyrgleuglumpglyserfroarg

AGENCOURT_14018626 NIH MGC 179 Homo IMAGE:30367261 5', mRNA sequence. CD106442

mRNA sapiens

linear cDNA clone

CD106442.1 EST.

GI:30759616

166 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu

62 562 165 502

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/ Lab_bose" PRION_TOTA } ( T and T5 phage resistances) *

/ Lab_bose" PRION_TOTA } ( T and T5 phage resistances) *

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1. (bases to object inh. gov/, Willied Chep;/Msg.upi.nh. gov/, Willied Chep;/Msg.upi.nh. gov/, Wational, Institution of Health, Mammalian Gene Collection (MGC)
404
                                                             106 ServalPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 125
                                                                                                                                344 CTGCTCCGCATCTCCCTGCTGCTCATCCAGTGGTGGCTGGAGCCCGTGCAGTTCCTCAGG
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                                                                                                                                                                                                                                                                 284 TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCCAACCTAGAG
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CDM Library Arraywad by The In A.G.E. Consortium (LIML)

CDM Albrary Grand Arraywad Corporation

DM Asquencing Appareoust Bioactence Corporation

Clone Chiefibelion MCC clone distribution information can be

cound bybrough to I.M.A.G.E. Consortium/LIML at:
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Tissue Procurement: Dr. Michael Brownstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
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Plate: NDAM428 row: c column: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTrp 20
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AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA 463
                                                                                                                                                                                             LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg
                                                                                                                                                                                                                                                                                                                              SerGluSerIleProThrProSerAsnArgGluGluThrGlnGlnLysSerAsnLeuGlu 85
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Location/Qualifiers
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//All Desired Hill Control (1) C
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/clone="IMAGE:30367261"
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CDM Library Arrayed by The II M.A.G.E. Consortium (CLNL)
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Tissue Procurement: Dr. Michael Brownstein
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National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Gaps: Conservative: Mismatches: Indels:

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                                                                                                                                                 Plate: NDAM428 row: d column:
                                                                                                                                                                                                                                                                                                                                                            Email: cgaphs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                    ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe
                                                                                                                                                                                                                                                                         AlaLeuLeuLysAsmTyrClyLeuLeuTyrCysPheArgLysAspMecAspLysValGlu 185
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ALIGNMENTS

NAIternate namme: growth hormone 1; hdH-N; pituitary somatotropin N; Ontains: growth hormone S; peptide; somatotropin 1, long form; somatotropin 1, chort c; Species: Homo aspinns (man) somatotropin 1 precursor [validated] - human

CDBern 24-Apr-1988 desegments revision 16-Pab-1985 stear change 00-331-2004 (Abecasion 19373) A3325 A33254, A34254, A3

A, Residues: 1-217 < DEN> A; Molecule type: DNA

A,Residues: 1-217 <CHE> A, Molecule type: DNA

ACCome-references UNISMIT-POIATA (pg. 19550)
AbSter the 20% Abort Come sensorogich ladds residues 58-72 (32-46 in the active borno
AbSter the 20% Abort Come sensorogich ladds residues 58-72 (32-46 in the active borno
Booken, F., Liao, Y.C.; Smith, D.H.; Burrers-Saldana, H.A.; Onlines, R.E.; Beeburg, P.
Accessorom (1988) Abort Come and R,Roskam, W., Rougeon, A;Cross-references: GB:J03071; NID:g183148; PIDN:ANA52549.1; PID:g183149 A;Accession: A32435

Nucleic Acidis Res. 7, 206-120, 1979 A/TLICH Molocular closing and nucleocide sequence of the human growth hormone structure A/Reference number: A93694, MUID:80034477, PMID:386281 A, Molecule type: mRNA

A,Residues: 1-217 <ROS>

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A;Accession: A90051 A;Molecule type: protein Rid, C.H., Dixon, J.S.
Arch, Blochem, Blodyn, 146, 233-236, 1971
Arch, Blochem, Blodyn, 146, 233-236, 1971
Aritide: Beams pitulity; growth Morkous. MAXII. The primary structure of the hormone: April Beams pitulity; growth Morkous. MAXII. The primary structure of the hormone: Applications of the Morkous. Applications of the Morkous. Maximum and Applications of the Morkous. Applications of the Morkous. Maximum and Applications of the Morkous. Ma

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A, Title: Revised primary structure for human growth hormone.
A, Reference number: A93397, MUID:71139765, PMID:5279046
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R;Niall, H.D.
Nature New Biol.
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Akmatenia (1973) Bonesald, L.F.; Levis, L.J. 1990
Bacohen, Biophys, Res Commun. 92, $11-516, greet bormone; location
AyTile: The 20,000-dalton variants outset protein bormone; location
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Riberdey, Ta.A., Daton, J.S., Lid. C.H.
Int. J. Pept. Process Res. 4, 281-287, 1972
A.Tit. Sequence companion of human pituitary growth hormone,
A.Title: Sequence Companion of human pituitary growth hormone,
A.Reference mumber: A91764, MUID:73092028; PMID:4678484
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A, Residues: 119-120, 157-159 <NI2>
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                                                                                  A, Title: Periplasmic production of correctly processed human A, Reference number: 44126; MUID:8613739; PMID:391261 A)Accession: 18459
A, Status: preliminary; translated from GB/BMBL/DDBJ
A, Status: preliminary; translated from GB/BMBL/DDBJ
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Side Yos, J.M.; Ultrebly, W. Komatacott. A.A.
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Alcohenter, M. Side Y. S. S. McKhown, K.S.; Haynaker, H.L.; Chang, C.S.
Godey, C.L.; Baltatidgs, J.S.; McKhown, K.S.; Haynaker, H.L.; Chang, C.S.
Geng, G.L.; Baltatidgs, J.S.; McKhown, K.S.; Haynaker, H.L.; Chang, G.S.
A,MOJecule type: mRNA
A,Mosedues: 1-26 cR895
A;Coses-references: GB:M14398; NID:g183158; PIDN:AAA52554.1; PID:g183159
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3 Robanon, VRAJ, Fas, 113, MAJ,
8501. Chem. Hoppe-Septide of the assurtistide etructure in a previously-reported peptide.
A.Tillit (dentification 50865; MUID-90314745; PMID:279879
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A; Residues: 27-69 <SIN>
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7. Protein Chem. 2, 425-436, 1983
1,Title: Human growth hormone peptide 1-43: isolation from pituitary glands
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Sudcerinology 133, 1744-1792, 1939
Agricus Closing of Econ growth homson-doctionic somatomamotropin-related complementary
Application under 173267; MID:9408724; MID:9408617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.LL, C.H., Chung, D.; Lahm, H.W.; Stein, S.
Arch. Biochem. Biophys. 245, 287-291, 1386
A,Fitte: The primary etrocure of monkey pituitary growth hormone
A,Reference number: A05094; MUID:86129460; PMID:3080959
                                                                                                                                                                                                                                                                                                                                           R;Raben, M.S.
Science 125, 883-884, 1957
A;Title: Preparation of growth hormone from
                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Molecule type: protein
A, Residues: 27-99, 'Q', 101-178, 'D', 180-217 <LIC>
A, Note: the monkey species is not identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P33093; GB:L16556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-217 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Accession: 167410
                                                         Ś
                                                                                                                                                                                                                                                        C;Superfamily: prolactin
                                                                                                                                                                                                                                                                                 A, Contents: annotation, identification
                                                                                                                                                                                                                                                                                                                 A; Reference number: A44774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A05094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: translated from GB/EMBL/DDBJ
                                                                                                                        Matches 193;
                                                                                                                                                                                        Query Match
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Local Similarity

Conservative

93.74,

Score 981. Pred. No.

of BOUTCE 4.96-82;

pituitaries of man and monkey

the reference organism

NID:g293114; PIDN:AAA18842.1; PID:g293115

09-Jul-2004

1 MATGSRTSLILLAFGLLCLFWLQEGSAFPTIFLSRLFDNASLRAHRLHQLAFDTYQEF--- 57

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Chayoran i transito apiating homens; pitutary
Chayoran in ten aegunes suctuu predicted adepartmental edul-
27-21/Podober; sommeteropin i, long form seatum separemental edul-
27-21/Podober; sommeteropin i, long form seatum separemental edul-
27-21/Podober; sommeteropin i, long form seatum separemental
27-21/Podober; sommeteropin i, nort form seatum separemental
27-21/Podober; sommeteropin i, meter se operatematal
27-21/Podober; sommeteropin i, seatum separemental
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A,Introns: 4/1; 57/3; 97/3; 152/3
C,Superfamily: prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GDB:119982; OMIM:139250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Gene: GDB:GH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Comment: The g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The gene for this bormone is transcribed only in sometotrophic cells of the about 90% of sometotropin is the 22K long form.
                                                166
                                                                                                                                                106 SVFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD 165
                                                                                                                                                                                                      61 YIPKEQKYSPLQNPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLR 120
                                                                                                                                                                                                                                                                 88
                                          ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF 202
                                                                                                                                                                                                                                                      -----NPQTSLCFSESIPTPSNREETQQXSNLELLRISLLLIQSWLEPVQFLR 105
                                                                                                                                                                                                                                                                                                                 MATGSRTSLLLAFGLLCLPWLQEGSAFPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEA 60
                                                                                                                                                                                                                                                                                                                                                                  MATGSRTSLLLARGLICLEWIQEGSAFFTIPLSRLEDNASLRAHRLHQLAFDTYQEF---
ALLKNYGLLYCPRKDMDKVETPLRIVQCRSVEGSCGF
                                                                                                     SVPANSLVYGASDSNVYDLLKDLEBGIGTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD 180
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1024.5; DB 1;
Pred. No. 5.9e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 217
                                                                                                                                                                                                                                                                                                                                                                                                                                        15,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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C.Reywords: alternative oplicing; glycoprotein; hormone; placenta
F)1-26/Domain: signal sequence Metatus predicted <SIG>
F)27-217/Product: sematotropin 2, long splice form Matatus predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A/Coose-references (Bais9451 NID)433179; PIDN:AAA35891.1; PID:9183180

R.Frankommer, F. despos, M.L. van Bewans, O. J. Jouc. A.; Bennen, G.

A/ILLes Identification tenab 71, 15-18 3380 J. J. 2001. A.; Bennen, G.

A/ILLes Identification of placeral human occurb hormane as the growth

A:Reference number: A60711; MUID:90317018; PMID:2196278
                                                                                                                           C/Superfamily: prolactin
                                                                                                                                                             A; Map position: 17q22-17q24
A; Introns: 4/1; 57/3; 97/3; 152/3
                                                                                                                                                                                                                           A;Gene: GDB:GH2
A;Cross-references: GDB:119983; OMIM:139240
                                                                                                                                                                                                                                                                                                                          A; Experimental source: tissue placenta A; Note: partial glycosylation was demonstrated by C; Comment: This gene is expressed by the placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Accession: A60711
A:Molecule type: protein
A:Residues: 27-44:46-57 <FRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R. Hagout, A., Beippo, M.J., Frankenne, F., Hennen, G.
Arch. Int. Physical Blochts 150, 657, 1889
A.Title: Cloning and mucleanists, 65, 1809
A.Reference maker: 182104, MUD.88024944, PMID.2460050
A.Reference in 152104
                                                                                                                                                                                                                                                                                                             C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/ENBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-217 <IGO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-34, 'P', 36-217 <SES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A/Accession: A01511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A/Coom-references UNIPSOT:POLYA/: OB.A/DVD7; NID:gl43148; FIDN:AAA55552.1; R(Cooke, N.E.; RAW, J.; Beary, J. (a), ideababer, S.*, A. (Colem. 26), 9001.900; 1988 and Joseph Borence-variant mask in the human growth borence-variant mask in the human firestence number: A92725; MUID:88243769; PUID:3179557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-217 < CHB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: mRNA
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C,Superfamily: prolactin
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F:27-57/3-211/Product; semetotropin 2, where splice form Waratus predicted <505:
E/79-191.208-215/inufide bondin: Waratus predicted the first predicted comparison of the first predicted first first
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Local Similarity
MATGSRTSLLLAFGLLCLFWLQEGSAFFTIPLGRLFDNASLRAHRLHQLAFDTYQEF---
                                 Conservative
                                          89.74;
                               4; Mismatches
                                          Score 939.5,
Pred. No. 3.3
                                       .3e-78;
                                                   DB 1;
                               Indels
                                                Length
                            15;
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MAAGSRTSLLLAFGULCISWLOBGSAFFTIFLSRLEDNAMLRARRLYQLAYDTYQEFEEA 60

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106 SVFANSLYYGASDSNYYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD 165 YILKEOKYSFLONPOTSLCFSESIPTPSNRVKTQQKSNLELLRISLLLIQSWLEPVQI LR 120

166 ALLKNYGLLYCFRKOMDKVETFLRIVQCRSVEGSCGF EDGSPRTGQIFNQSYSKFDTKSHNDD 180

217

choriomammotropin B precursor - human names: chorionic somatomammotropin

C:Species: Homo sapiens (man) C:Date: 29-Dec_1389 #sequence_revision 29-Dec-1989 #text_change 09-Jul-2004

A; Title: The human growth hormone locus: nucleotide sequence, A; Reference number: A32435; MUID:89307277; PMID:2744760 C;Accession: E32435 R;Chen, E.Y.; Liao, Y.C.; Smith, Genomics 4, 479-497, 1989 D.H.; Barrera-Saldana, H.A., Gelinas, biology, and R.B.; evolution Seeburg,

A;Cross-references: UNIPROT:Q14407; GB:J03071; NID:g183148; PIDN:AAA52553.1; PID:g18315

A;Cross-references: GDB:119813; CMIM:11882

Similarity Conservative 83.4%; Score 873.5; DB 79.3%; Pred. No. 3.4e-72 Mismatches 2 Indels Length 217; 15,

Gaps

1 MATGSRTSLILLAFGLLCLPWLQEGSAFPTIPLSRLFDNASLRAHRLHQLAFDTYQEF---MAGGRTSLLLAFALICIPHIQEAGAVQTVPLSRLFDHAMIQAHRAHQIAIDTYQEFEET 60

SMFANNLYYDTSDSDDYHLLKDLBEGIQTLMGRLEDGSRRTGQILKQTYSKFDTNSHNHD SVFANSIVYGASDSNVYDLLKDLEGGIQTIMGRLEDGSBRTGGIFKQTYSKFDTNSHNDD

180 165 120 105

217

choriomammotropin A precursor [validated] - hur N;Alternate names: chorionic somatomammotropin C:Species: Homo sapiens (man) placental lactogen

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Charce 23-Oct-1981 Hedgazer, gwisian 25-Oct-1981 Hedga 25-Oct-1981 Hedga 25-Oct-1981 Company (20-Oct-1981) 159239, 755 Chocas 25-Oct-1981 Company (20-Oct-1981) 159239, 755 Chocas 25-Oct-1981 Chocas 25-Oc
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R. Shine, J.; Semburg, P.H. Martial, J.A.; Baxter, J.D.; Goodman, H.M.
R.Shine, J.; Semburg, P.H. Martial, J.A.; Baxter, J.D.; Goodman H.M.
Nature 270, 94-98, 349 analysis of recombinant DNA for human chorionic
A;Filter Commercetion analysis, MSISSI, MSID:78071761; PMID:593368
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Bistophen Sec. Trans. 15, 200, 1981
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Ajriles Section 18, 2003
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R;Li, C.H.; Dison, J.S.; Chung; 10, 1973
Arch, Bloches, Bisonesso de basan chorionic somscomamorropin
A;Tkler Matto acid softwares of basan chorionic somscomamorropin
A;Reference annoc; 80054; WID:73201971; PMID:4712450
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A;Residues: 1,3-26 <SHE>
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A;Accession: A94427
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A;Residues: 50-217 <SHI>
A;Contents: annotation
R;Sherwood, L.M.; Handwerger, S.; McLaurin,
Nature New Biol. 235, 64, 1972
                                                                                                                                                                                                              A;Title: Amino-acid sequence of human placental lactogen
A;Reference number: A93401; MUID:72016313; PMID:5286363
                                                                                                                                                                                                                                                                                                                                                  A; Note: choriomammotropin apparently copurified with placental decchol-O-methyltransfor, R.Shenvood, L.M.; Bandewayer, S.; Ecawith, W.D.; Lammer, M. Kente, See Soil, 1331, S. 541, 1911.
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Residues: 1-3 <TAN>
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Residues: 27-217 <LIC>
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                                                                                                                     W.D., Lanner,
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A;Map position: 17022-17024
A;Introme: 4(1: 57/3; 97/3; 152/3
A;Introme: 4(1: 57/3; 97/3; 152/3
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C;Superfamily: prodectin
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A; Residues: 1-217 < RES>
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Nitita Conding of Cour growth Magazana/Continuis scentrammotropin-related complementary Agence mander; 153247, MID:4408724; MID:8408617
Ajectementary (153247) MID:8408724; MID:8408617
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A;Residues: 160-217 <RE2>
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(Specia: Hearts) - Freuru Ancaque

(Specia: Hearts) - Hearts Ancaque (Principale: 13-May-1996 #rext_change 09-Ull-2004

(Specia: 13-May-1996 #requence_revision 31-May-1996 #rext_change 09-Ull-2004

(Specia: 15-Ull-Unring, M., Fishber, J.M.) Fowler, P.D.
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    Mismatches
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Length 217;

#status experimental 15; Gaps

A; Reference

A93405

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Accelents amounted to Monabel, K.; Busell, J.; Sherwood, L.M. Basimander, A.B.; Owanabel, K.; Busell, J.; Sherwood, L.M. Basimander, A.B.; Owanabel, K.; Basimander, A.B.; Owanabel, C. B. Basimander, A.B.; Owanabel, C. B. Basimander, A.B.; Carlonia, C. B. Basimander, C. Basimander, C. B. Basimander, C. B. Basimander, C. B. Basimander, C. Bas
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Indels Length

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R.Golois, T.G., burning, M.; Fisher, J.M.; Fowler, P.D.
Bedocricology, 33, 1744-1752, 1993
Arfitle. Closing of four growth hormone/chorionic sematosammotropin-related
ArReference number: 183857; MUID:94008724; PMID:9404617
                                                                                                                                                                 #Constotropin - rhesus macaque
W.Alternate names: growth hormone
Cispociem: Monaco milatra (thesus macaque)
Cispociem: 31-May-1996 #sequence_revision 31-May-1996 #text_
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RODOS T.G.; Doning M.; Felber, J.M.; Fowler, P.D.

RODOS T.G.; Doning M.; Felber, J.M.; Fowler, P.D.

RODOS T.G.; Doning M.; Fowler, P.D.

RODOS T.G.; DONING M.; Fowler, P.D.

Alecession units of Control of Cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ciberionic somatomammotropin-1 - rhesus macaque
C:Species: Mecade mulatta (thesus macaque)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #rext_change
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C:Superfamily: prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YIPKEKKHSIMENÞÓNSFÓFADSÍÞÝÞSNIÆÐTÓÓKSNIÆLLRÍSLÍLLÍÓSMLEÐVOÐLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVFANNLLHHTSDSDVHDLLKDLEBGIETLAWRLEDGIFRTGHIFKGTYSKFDAHSONDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SILKNYBILHCFRKDMDMVETFLRMVQCRTVEGSCGF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVEANSLYZGASDSNYYDLLXDLESGIQTLAGRLEDGSBRTGQIFKQTYSKFDTNSHNDD 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YIPKEKKHSLMGNPQASFCPSESIPTPSNREETQQKSNLELLRISLLIQSNLEPVQLLG 120
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75.61;
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77.4%; Pred. No. 1.5e-71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 850.5; DB 2;
Pred. No. 4.3e-70;
8; Mismatches 20;
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                                                                                                                                                                                                                                                                                                                                                                                             217
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                                                                                                                                                                      _change 09-Jul-2004
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Chbrindte scaatomsmmotropin-2 - rhesus macaque (fragment)
C:Species; Nacuca mulatta (thesus macaque)
C:Date: 31-My-1996 Secquence_revision 31-May-1996 Stext_change
C:Accession: 167408
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DNA 6, 59-70, 189
A.Title: The human growth hormone gene locus: structure,
A.Reference number 226449, MUID:07161235; PMID:0303080
A.Paccematon: 226449
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F;1-26/Domain: signal sequence #status predicted <SIG>
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A; Residues: 1-215 <HIR>
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C:Speciae: June appears (man)
C:Dete: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Mccassion_A2649
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C:Superfamily: prolactin
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A;Status: preliminary; translated from A;Molecula Cype: mRNA
A;Residues: 1-217 <RES>
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                                                                                                                                                                                                                 ALLKNYGLLYCFRKOMDKVETFLRMVQCRSVEGSCGF
                                                                                                                                                                                                                                                                                                  SHFANNLVYDTSDSDDYHLLKDLEBGIQTLMGRLEDĞSRRİĞĞİLKĞİYSKEDİNSHNHD 178
                                                                                                                                                                                                                                                                                                                                                                                                                        YIPKDQKYSFLHDSQTSFCFSDSIFTPSNMEETQQKSNLELLRL
                                                                                                                                                                                                                                                                                                                                                             SVFANSLYYGASDSHYYDLLKDLEEGIQTLMGRLEDGSPRTQQIFKQTYSKFDTNSHNDD 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Magsrtslillafallclfmlgeagavotvplsrlfdhamigahraholaidtygefeet
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77.9%; Pred. No. 2.3e-69;
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Pred. No. 1.9e-69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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Ridolop, T.G.; Darning, M.; Fisher, J.M.; Fowler, F.D.
Miltita, Cduffing, Of Four growth borsons (shorionic semicomamotropin-related complemental
A. Reference number: 15367; MUID:3400974; PMID:444617
A. Agencence., 157:06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Accession: B32435 y.C., Smith, D.H.; Barrera-Saldana, H.A.; Gedinas, R.E.; Seeburg, R.Chon, E.Y.; Liao, y.C.; Smith, D.H.; Barrera-Saldana, H.A.; Gedinas, R.E.; Seeburg, Gancinics 4, 4(7)-4(7), 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                choriomammotropin-like protein precursor - human
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A. Rossiones: 1-195 (MIREO
A. Cross-references: UNIREO
A. Cross-referably: PODJACTIA
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A, Reference number: A32435, MUID:89307277, PMID:2744760
A, Accession: B32435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Homo sapiens (man)
C:Date: 29-Dec-1989 #sequence_revision 29-Dec-1989 #text_change 09-Jul-2004
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178
                               181
                                                                                                                                                                                                                                                                         157
                                                                                                                                 61 WCM---DSIPTSSNMESTÇOKSNLELLHISLLLIESRLEPVRFLKSTFTNNLVYDTSDSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLVYGASDSNYYDLLKDLEBGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDDALLKN 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKHSLMENPOASFCPADSIPTPSNLEETQOKSNLELLRISLLLIQSWLEPVQFLSSVPAN 120
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                                                                                                                                                                    TSLCFSESIFTPSNREETQQKSNLELLRISLLLIQSWLEPYQFLRSVFANSLVYGASDSN 120
                                                                                                                                                                                                                                      MATGSRTSLLLAFGLLCLPWLQEGSAFPTIFLSRLFDNASLRAHRLHQLAFDTYQEFNFQ 60
                                                                                                 VYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDDALLKNYGLLYCFRKD 180
                                                                                                                                                                                                      MAAGSRTSULLAPALLCLPWLQEAGAVQTVPLSRLPKEAMLQAHRAHQLAIDTYQEPISS 60
MDKVETFLRMVQCRSVEGSCGF 195
                               MDKVETFLRIVQCRSVEGSCGF 202
                                                                  DYHLLKOLEEGIQMLMGRLEDGSHLTGQTLKQTYSKFDTNSHNHDALLKXYGLLHCPRKD
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Pred. No. 2.2e-68;
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                                                                                                                                                                                                                                                                                                                   Length 199;
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                                                                                                     A, Molecule type: mRNA
A, Residues: 1-216 <KAT>
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A, Residues: 1-216 <VIZ>
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NyAlternate names: growth hormone
Cispeciae: Oanis lupus familiaris (dog)
Cispecia: 13-pec-1997 Heequence_revision 19-bec-1997 #text_change 09-Jul-2004
CiAccession: 166145, 355790
CiAccession: 166145, 355790
Rigacato-Martines, J.A.; Barrera-Saldana, H.A.
protein identical to
                     pig growth hor
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A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: 1-216 <ASC> A;Cross-references; UNIPROT:pl3711; EMBL:223067; NID:g312195; FIDN:CAA80601.1; FID:g31211 A;Rober; Submitted to the BMBL Date Library, June 1993 A;Title: A dog growth hormone cDNA codes for a mature F A;Reference number: I46145; MUID:94266166; PMID:8206387

C;Kejwords: hormone; pituitary Fil-26/Domain: signal sequence #status predicted <8IG> Fil-26/Domain: signal sequence #status predicted <8MT> Fig-216/Product: sematotropin #status predicted F;78-189,206-214/Disulfide bonds: #status predicted Superfamily: prolactin

Local Similarity 140; MATGSRTSLILLAEGILCLEWLQBGSAEPTIPLSRLEDNASLRAHRIHQLAEDTYQBE---Conservative 64.5%; 20; Mismatches Score 698; DB 2; Pred. No. 3.4e-56; Length 216; Indels Gaps

YIPEGORYSIQNAQAAFCFSETTFAFTGKDBAQQRSDVELLKFSLLLIQSWLGFVQFLSR 120 MAAGPRTSVLLAPALLCLPWPQEVGAPPAMPLSSLPANAVLRAQHLHQLAADTYKEFERA 60 VPANSLYYGASDSNYYDLLKDLEEGIQTLAGRLEDGSPRTGQIFKQTYSKFDTNSHNDDA 166 -----NEQTSLCESSIPTESNREETQQKSNLELLRISLLLIQSWLEEPVQFLRS 106

LLKNYGLLSCFKKDLHKAETYLRVMKCRRFVESSCAF 216 LIKNYGLIYCFRKDMDKVETFLRIVQCRS-VEGSCGF 202

C.Species: sus scroft domestic Dis) Cobet: 9-0-01-1992 isoquence_revision 10-010-1992 Heat_change 09-011-2004 C.Accession: WOLD: 850035; 14654; 14658-; PC166) ANIŠir; A04594 R.Yaze, P.D., Wolls, U.S. Geng 55, 139-34; 1367 somatotropin precursor - pig N;Alternate names: growth hormone

A; Title: Isolation and characterization of A; Reference number: JW0015; MUID:88030700; the porcine growth hormone PMID:3666458

Al Cicomo referencies: 'Dirpoor, P02246; Om; MC7704; NID-p164475; PIRM-ANAIS44.1; PID-p164475; Riktor, V.; Shinokawa, N.; Wakasa, W.; Maran, W.

DNA 2. 37.45, 1983 A,FRIFIG: Efficient bacterial expression of bovine and porcine A,FRIFIG: mumber: 145898; MUID:83209123; PMID:6303731 R;Seeburg, P.H.; Sias, S.; Adelman, J.P.; de A;Cross-references: GB:X53325; NID:g288361; PIDN:CAA3741171, PID:g288362 R;Seeburg, P.H.; Sias, S.; Adelman, J.P.; de Boer, H.A.; Hayflick, J.; J

growth hormones. J.; Jhurani, P.;

AjAccession: 146584), translated from GB/RMBL/DDBJ AjKatelus preliminary, translated from GB/RMBL/DDBJ AjKateldus typs: March 121, (O. 23-216 48E5) AjKateldus Fris, W. 122, (O. 23-216 48E5) AjKateldus Fris W. 122, (O. 23-216 48E5) AjKateldus Fris W. 122, (O. 23-216 48E5)

RESULT 12 I46145

somatotropin precursor - dog

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W.Alternote hames; growth bonnese
G.Spection Falls at Youngia Could (Generic cat)
G.Spection, 721396 Hespance_mvision 24-May-1396 Heavt_change 09-Jul-200
G.Marshiam Jodgsia,
G.A. Begenson, 6.
A. Filter Closing of the Codes occlude for cat growth hormone and prolactin.
A. Filter Closing of the Codes occlude for cat growth hormone and prolactin.
A. Filter Closing of Jodgsia, MILD:96199806; PMID:863953
                                                                                                                                                                               JC4632
                                                                                                                                                   somatotropin precursor - cat
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gMills JB, Howard, SC, Scape, S.; Wilhelmi, A.E.
A/ELDA, Come, 245, 2407-2415, 1370
A/ELDA, Come, 245, 2407-2415, 1370
A/Elda Resource makes broaded cleaves and partial main acid segments of porcine growth
A/Edcamaton makes (A/ESS) MUID/70233161; MUID/913120
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A; Residues: 140-148 <MIZ>
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A;Residues: 27-30;149-194,'N',196-216 <MIL>
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A; Residues: 97-108, 'B', 110-158 < YAN>
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Best Local !
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27-216/Product: sommtouropin Metatus predicted <830s
27-216/Product: sommtouropin Metatus predicted
48AT-
78-189/Disulfide bonds : Metatus experimental
206-214/Disulfide bonds: Hetatus experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: prolactin
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A.Reference number: I46585; MVID:89137997; PMID:3224824
A;Accession: I46585
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                                                                                                                                                                                                                                                                                                                            VFANSLYYGASDSNYYDLLKDLEEGIQTLMGRLEDGSPRTOQIFKQTYSKFDTNSHNDDA 166
                                                                                                                                                                                                                                                                                                                                                                   YIPEGORYSIQNAQAAFĆFSETIPAPTGKDEAQORSDVELLRPSLLLIQSWLGPVOFLSR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MATGSRTSLLLAFGLLCLPWLQEGSAFPTTPLSRLFDNASLRAHRLHQLAFDTYQEF---
                                                                                                                                                                                                                                    LLKNYGLLSCFKKDLHKABTYLRVMKCRRFVESSCAF 216
                                                                                                                                                                                                                                                                                                                                                                                                      -----NPQTSLCFSBSIFTPSNREETQQKSNLELLRISLLLIQSWLEPYQFLRS
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64.1%; Pred. No. 7.8e-56;
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A;Reference number: $49483
A;Accession: $49483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generatoryin preparator - rabbit
Whitemente masses proposed bornous
Cispecies (Oryccologus cumicatus (domestic rabbit)
Cispecies (Oryccologus cumicatus (domestic rabbit)
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A; Residues: 1-216 <WAL>
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A;Residues: 1-216 <MRRs
A;Cross-references: UNIPROT:P46404;
A;Experimental source: pituitary
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                               ;Genetics:
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C; Keywords: pituitary
                                                                                                                                                                                                                                                                                         Matches
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Similarity 63.1%;
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GB:U25973; NID:g825768; PIDN:AAA67294.1; PID:g825

predicted AMAT' Length

<SIG:

Score 687; DB 2; Pred. No. 3.4e-55; 0; Mismatches 43 Indels 16; Gaps

MAAGPRNSVLLAPALLCLPWPQEVGTFPAMPLSSLPANAVLRAQHLHQLAADTYKEFERA 60 MATGSRTSLILLAFGLLCLPHLQEGSAFPTIPLSRLFDNASLRAHRLHQLAFDTYQEF---100 57

VPANSLYYGASDSNYYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDDA YIPEGGRYSIQNAQAAFĆĖŠĖTIPAPTGKDĖAQQRSDVELLRESLLLIQSWLGDVQFLSR 120 -----NPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLRS 166

VFTNSLVFGTSD-RVYEKLKDLEEGIQALMRELEDGSPRGGQILKQTYDKFDTNLRSDDA 179

LLKNYGLLSCFKKDLHKAETYLRVMKCRRFVESSCAF

for rabbit growth hormone

EMBL:238127; NID:g558682; PIDN:CAA86287.1; PID:g558

Score 682; DB 2; Pred. No. 9.7e-55; Length 216 Indels 16;

Gaps

107 VFANSLYYGASDSNYYDLLKDLEBGIQTIMGRLEDGSPRTGQIFKQTYSKFDTNSHNDDA 166 YIPEGORYSIOMOAAFCESETIPAPTGKDEAQQRSDMELLRESLLLIGINGTHINGISRJGPVQFLSR ------NPOTSLCFSESIFTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLRS 120

LLKNYGLLYCFRKDMDKVETFLRIVOCRS-VEGSCGF

Search completed: February 6, 2005, 13:05:12 Job time : 40 secs

Regult

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Match

Sequence 1

Score 1029.5 1029.5 1029.5

US-10-788-318-3 US-09-804-409A-17 US-10-411-037-47 US-10-411-026-47 US-10-410-962-47

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Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seg length: 2000000000
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Copyright (c) 1993 - 2005 Compugen Ltd.
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> US-10-621-693-67 US-10-621-693-65 US-10-621-693-65 US-10-311-473-9 US-10-311-473-8 US-10-311-693-1 US-10-794-615-14

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                        Sequence 1, Application US/9953689
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APELICANT: GEOGREE, DAVID N.
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CURRENT APPLICATION NUMBER: US/09/853,688
CURRENT FILING DATE: 2001-05-14
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                                                            Sequence 1, Application US/10788318
publication No. US20040137510A1
GENERAL IMPORMATION.
APPLICANT: COOPER, DAVID N.
APPLICANT: PROCTER, ANNIE M.
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RESULT 4 US-10-788-318-3

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166 AlaleuleulysAsnTyrGlyLeuLeuTyrCysPheArglysAspMetAspLysValGlu 185

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ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACCTCACACAACGATGAC ThrGlyGlnIlePheLysGlnThrTyrSerLysPheAspThrAsnSerHisAsnAspAsp AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG LysAspLeuGluGluGlyI1eGlnThrLeuMetGlyArgLeuGluAspGlySerProArg AGTOTOTTOGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA ServalPheAlaAsmSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu TROTTCOGGATCTCCCTGCTGCTCATCCAGTCGTGGAGCCCGTGCAGTTCCTCAGG

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US-09-856-796B-2 (1-202) x US-10-788-318-3 (1-654)
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LENGTH: 654
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CURRENT FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 66
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NAME/KEY: CDS
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ORGANISM: Homo
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                                   TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAACCTAGAG
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US-09-804-409A-17
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Patent No. US20020155100A1
GENERAL INFORMATION:
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SEQ ID NO 17
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APPLICANT CHEMA. ANTHONY T.

TITLE OF INVENTIONS COMPOSITIONS AND METHODS FOR REGULATED PROTEIN
TITLE OF INVENTIONS COMPOSITIONS AND METHODS FOR REGULATED PROTEIN
TITLE SETEMBORG. CO2996/CD3 8731.

THILE REFERENCE. CO2996/CD3 8731.

CHEMAT REPLICATION MORBERS US/90/804,409A

CHEMAT RELIGIO FATE. 2001-03-12

NUMBERS OF SEGIO 10 802-18
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                                  *166 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysBheArgLysAspMetAspLysValGlu 189
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                                                                                                                                                                        ANGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG
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ThrGlyGlnIlePheLysGlnThrTyrSerLysPheAspThrAsnSerHisAsnAspAsp
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US-10-411-037-47
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Publication No. US20040043446A1
MEDICANT, CHAM, MI
APPLICANT SHORM CHARGESTANGE A REMODELING AND GLYCOCOMUMNITION OF ALFRA
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Zopf, David
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Hakes, David
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Percent Similarity: Best Local Similarity: Pred. No.: US-10-411-037-47 PRICE PLINE DATE: 2001-10-10
PRICE PLINE DATE: 2001-10-10
PRICE PLINE DATE: 2001-10-10
PRICE PLINE DATE: 2001-10-10
PRICE PLINE DATE: 2001-10-10
PRICE PLINE DATE: 2001-10-10
PRICE PLINE DATE: 2001-20-10
CE PLINE DATE: 2001-20
PRICE PLINE DATE: 2001-20
PRICE PLINE DATE: 2001-20 Alignment Scores SEQ ID NO 47 SOFTWARE: PatentIn version 3.2 ORGANISM: Homo sapiens ENGTH: 799 1.1e-127 1017.50 92.17* 92.17* 97.18* Matches: Mismatches: Conservative:

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US-09-856-796B-2 (1-202) x US-10-411-037-47 (1-799)
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Gaps: Indel8:

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-- AsnProGlnThrSerLeuCysPhe 65

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SerGluSerIleProThrProSerAsnArgGluGluThrGlnGlnLysSerAsnLeuGlu

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US-09-856-796B-2 (1-202) x US-10-411-026-47 (1-799)
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 47
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PRIOR PILING MARE 2001-10-10-10/344,692
PRIOR PELICATION MUNERS US 60/344,692
PRIOR PELICATION MUNERS US 60/397,292
PRIOR PILING MARE 2002-6-07
PRIOR PILING MARE 2002-6-07
PRIOR PERIOR MEMBERS US 60/391,777
PRIOR PERIOR MEMBERS US 60/391,777
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Publication No. US20040063911A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PROFEST REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY
TITLE OF INVENTION, NETHODS
THE REFERENCE: 04083-01-5553
CURRENT ETLING DATE: 2003-04-09
CURRENT ETLING DATE: 2003-04-09
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                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
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Hakes, David
Chen, Xi
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                    FRIOR APPLICATION NUMBER: US 6/7/20, 523
PRIOR FILMED DATE: 2001.50-1,
PRIOR FILMED DATE: 2001.50-1,
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PRIOR FILMED DATE: 2002.06-0,
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Publication No
                                                                                                                                                                                                                                                                                      ITILE OF INVENTION: GRANUSCYTE COLONY STIMULATING PACTOR: REMODELING FILE REFERENCE: ORGES: 01:0500MUMATION OF G-CSF CHRENT APPLICATION NUMBER: US/10/410,962
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                                                                                                                                                                                                                                                                                CURRENT FILING DATE:
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APPLICANT: DeFrees, Shawn
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APPLICATION NUMBER: US &
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Bowe, Caryn
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Bayer, Robert
Hakes, David
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Best Local Similarity:
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PRIOR PILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS : 75
SOPTWARE: Patentin version 3.2
SEQ ID NO 47
LENGTH: 799
                                                                                                                         US-10-411-049-47
Sequence 47, Application US/10411049
Publication No. US200400822661
GENERAL INFORMATION
APPLICANT: Neose Technologies, Inc.
APPLICANT: Neose Technologies, Inc.
APPLICANT: APPLICANT: Applicant Applicant Applicant Applicant
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) ORGANISM: Homo sapiens
US-10-411-049-47
                 Best Local Similarity:
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Pred. No.:
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LENGTH: 799
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CURRENT FILMS DATE: 2003-04-09
CURRENT FILMS DATE: 2001-04-09
PRIOR PILMS DATE: 2001-10-10
PRIOR PILMS DATE: 2001-10-10
PRIOR PILMS DATE: 2001-10-10
PRIOR PILMS DATE: 2001-10-10
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION MIMBER: US 60/387,292
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCOMJUGATION OF INTERFERON
TITLE OF INVENTION: ALPHA
1711E REFERENCE: 10:045:3-02-055.
                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
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                                                                                                                                                                                       TYPE: DNA
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Query Match:

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APPLICANT:

Bayer, Robert

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-AsnProGlnThrSerLeuCysPhe 65

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US-09-856-796B-2 (1-202) x US-10-410-997-47 (1-799)
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Best Local Similarity:
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Publication No. US20040132640A1
TITLE OF INSTITUTE (ACCESSITATION METHODS AND PROFESS/PERFIDES PROUCED INTELS OF INVESTIGES, CHEMICA S. (PRINCE)

FILE REFERENCE: CHOOSE-05-203, ////L1, 0.2

CHEMICA FILLING DATE: 2003-0-05

PRICE APPLICATION MYMERS: US 6/124-5/23

PRICE APPLICATION MYMERS: US 6/124-5/23

PRICE APPLICATION MYMERS: US 6/124-7-29

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PRICE APPLICATION MYMERS: US 6/124-7-29
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APPLICANT: Bowe, Caryne
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
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                               RESULT 13
US-10-287-994-47
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PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version 3.2
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PRIOR APPLICATION NUMBER US 60/391,777
PRIOR PILING DATE: 2002-06-25
PRIOR PILING DATE: 2002-06-25
PRIOR PILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER US 60/396,594
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                                                                                                                                                                            ThreheLeuArgIleValGlnCYsArgSerValGluGlySerCysGlyPhe 202
                                                                                                                                                                                                                                                        GCACTACTCAMGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCGAG
                                                                                                                                                                                                                                                                                                     AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu 185
                                                                                                                                                                                                                                                                                                                                                                                  ACTOGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC
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US-09-856-796B-2 (1-202) x US-10-287-994-47 (1-799)
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PRICE FLING DATE 2012-8-18 6/187,292
PRICE APPLICATION UNDERS US 62.6/191,777
PRICE FLING DATE 2012-6-26/191,777
PRICE FLING DATE 2012-6-71
PRICE FLING DATE 2012-6-71
PRICE FLING DATE 2012-6-18
PRICE MPPLICATION UNBERS US 67.404,249
PRICE MPPLICATION UNBERS US 6.16
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LENGTH: 799
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PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NIMBER OF SEC. T. 2002-08-28
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APPLICANT: DeFrees, Shawn
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AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA
                                       ServalPheAlaAsnSerLeuvalTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 125
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                                                                                                                                                                          LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg 105
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                                                                                                                                                                                                                                                                                                             SerGluserIleProThrProSerAenArgGluGluThrGlnGlnLysSerAenLeuGlu
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Chen, Xi
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Bowe, Caryn
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Bayer, Robert
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Query Match:
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PRICE PREVIOUS DATE: 2001-04-05
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US-10-410-913-47
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LENGTH: 799
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Publication No. US20040142856A1
                                                                                                                                                                                ORGANISM: Homo sapiens
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
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Bayer, Robert
Hakes, David
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		E	FILE REFERENCE: 425243 GURRENT APPLICATION NUMBER: US/10/477,651 CURRENT FILING DATE: 2003-11-14 CURRENT FILING DATE: PCT/US02/15172 PRIOR APPLICATION NUMBER: PCT/US02/15172	NUMBER: U 2003-1: MBER: PC	PILE REPERENCE: 223223 CURRENT APPLICATION NUMBER: 200 CURRENT FILING DATE: 200 CURRENT FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FIL	FILE REFEI	
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	AsnProGlnThrSerLeuCysPhe	AsnPro				58	§ :
AMGCC 220	CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGAAGAAGCC	TTGACACCTAC	CTCCGCGCCCATCGTCTGCACCAGCTGCCCTTTGACACCTACCAGGAGTTT	TCGTCTGC	CICCGCGCCCA	161	B 8
57	GlnGluPhe	heAspThrTyr	isGlnLeuAlaF	saroLeuH	rauargālaHi		?

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ificial Sequence

WION: Description of Artificial Sequence: DNA encoding WION: the mature human growth hormone, containing an WION: artificial XMaI site introduced by modifying WION: nucleotides at positions 21 and 24

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4.33e-118 1024.50 92.63% 92.63% 97.85%
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GENERAL INFORMATION:
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Patent No. 6410220
                                                                                COMPUTES ESDABLE FORM:

COMPUTES: INDEX PLOS PLANTS: LAMP PC COMPUTES: 1MM PC COMPUTES: 100, VOX.

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COMMANDER: PARENTIA PROPERTY APPLICATION MARKER: 105/9300.190A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAACACAACAGAAATCCAACCTAGAG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGGACCTAGAGGAAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATTGGCAGCCCCCGG
                                                         CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                    ZIP: 55401
                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THEREOF
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                                                                                                                                                                                 Version #1.30
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VECTORS AND USES
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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SEQUENCE CHARACTERISTICS:
LENGTH: 5594 base pairs
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ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2330 CTTCAAGAGGGCAGTGCCTTCCCAAGCATTCCCTTATCCAGGCTTTTTGACAAGGCTATG 2389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2270 Arederacionale de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya del companya de la companya de la companya del companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya del companya de la companya de la companya de la companya de la companya del companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya del companya de la companya de la companya de la companya del companya de la companya de la companya de la companya de la company
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 228.00010201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MUETING,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 612-305-1228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAACCTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerGluSerIleProThrProSerAsnArgGluGluThrGlnGlnLysSerAsnLeuGlu
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                                                                                                                                                                                                                                                AlaLeuLeuLyeAssTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu 185
                                                                                                                                                                                                                                                                                                                    ThrGlyGlnIlePheLysGlnThrTyrSerLysPheAspThrAsnSerHisAsnAspAsp 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCCTCTGACAGCAACGTCTATGACCTCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ServalPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLou 125
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                                                                                                                                         ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202
                                                                                                                                                                                                        GCACTACTCAACAACTACGGGCTGCTCTACTGCTTCAGGAAAGGACATGGACAAGGTCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LyshapLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 145
                                                                                     ACATTCCTGCGCATCGTGCAGTGCGCTCTGTGGAGGCAGCTGTGGCTTC 2920
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Indels:
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2569 2629

286 2809 2749 2689

US-09-380-190A-21

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US-09-856-796B-2 (1-202) x US-09-380-190A-21 (1-7080)
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
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Patent No. 6410220
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 612-305-1217
TELEPAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                   2968 CTCCGCGCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGAAGAAGCC 3027
3088 TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAACCTAGAG 3147
                                                               3028 TATATOCCAAAGGAACAGAAGTATTCATTOCTGCAGAACCCCÁGACCCTCCCTCTCTTTC 3087
                                                                                                                                                                                                                           2908
                                                                                                                                                                                                                                                                             2848 ATGGCTACAGGCTCCCGGACGTCCCTGGTCCTGGCTTTTTGGCCTGCTCTGCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                            66 SerGluSerIleProThrProSerAsnArgGluGluThrGlnGlnLysSerAsnLeuGlu 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/380,190A
                                                                                                                                                                                                                                      21 LeuGlnGluGlySerAlaPheProThrileProLeuSerArgLeuPheAspAsnAlaSer 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: NATURE TECHNOLOGY CORPORATION,
TITLE OF INVENTION: SELF-ASSEMBLING GENES,
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 74
                                                                                                                                                                                                                                                                                                                           -
                                                                                                                                                                   LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe-----
                                                                                                                                                                                                      CTTCANGAGGGCAGTGCCTTCCCANCCATTCCCTTATCCAGGCTTTTTGACAAGGCTATG 2987
                                                                                                                                                                                                                                                                                                          MetAlaThrGlySerArgThrSerLeuLeuLeuAlaPheGlyLeuLeuCysLeuProTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 7080 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 228.00010201
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FILING DATE: 28-FEB-98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING YSTER: PC-DS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
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92.63†
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                                                                                               ----AsnProGlnThrSerLeuCysPhe 65
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Mismatches:
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VECTORS AND USES
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			Human -2779	ORGANISM: Huma 09-949-016-2779	us-
	4.0	0000-09-08 2000-09-08 35: 207012 or Windows Version 4.0	DATE: Q ID NO stSEQ 1	ENGI DE MERCE	SEQUEN
		WMBER: 60/237,768 2000-10-03	APPLICATION NUMBER: FILING DATE: 2000-1		
		APPLICATION NUMBER: 60/241,755 FILING DATE: 2000-10-20	APPLICATION NUM FILING DATE: 20		٠. ٠.
	016	TOMBER: US/09/949,016	CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2000-	CURRENT API	٠. ٠.
ASSOCIATED OF DETECTION AND USES		FORMATION: VENTER, J. Craig et al. INVENTION: POLYMORPHISMS IN KNOWN GENES INVENTION: WITH HUMAN DISEASE, METHODS RENCE: CLOOLIO?	ENERAL INFORMATION: APPLICANT: VENTER, J. CY TITLE OF INVENTION: WIT TITLE OF INVENTION: WIT FILE REFERENCE: CLOO1307	GENERAL INFORMATION: APPLICANT: VENTER, TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: CLO	
		79 Application US/09949016 2339	-2779 79, Applica 6812339	RESULT 4 US-09-949-016-2779 ; Sequence 2779, App ; Patent No. 6812339	· · · · · · · · · · · · · · · · · · ·
GCTGTGGCTTC 3498	CTCTGTGGAGGGC	ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC		3448	망
GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGA	CTACTGCTTCAGG	AAGAACTACGGGCTGCT		186	\$ E
AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu	uTyrCyspheArg	LysAsnTyrGlyLeuLe		166	. 8
ACTGGGCAGATCTTCAGCAGACCTACAGCAGATTCGACACAAACTCACCACCACCACGATGAC	CAGCAAGTTOGAC	ATCTTCAAGCAGACCT		3328	B :
WANDENGLIGUINGLY11eGINThrLewherGlyArgLewGluAspGlySerProArg	nrLeuMetGlyArg	GAGGAAGGCATCCAAA		3268	? B 5
ServalPhallakmserlenvalTyrGlyAlaserAgpSerAgnValTyrAgpLeuLeu	CGGCGCCTCTGAC	AlaAsnSerLeuValT		3208	? F 5
HELLENDY 11 850 FLEUTENLEWIL BOINS STTPLEWGLUP FOWN TO INFINELEMENT THE WORLD THE WORL	leGlnSerTrpLeu	ATCTCCCTGCTGCTCA		w	? - 문 5
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123 CTTCAÁGAGAGGCAGTGCCTTCCCAÁCCATTCCCTTATCCAGGCTTTTTGACAACGCTATG 182

LeuGlnGluGlySerAlaPheProThrileProLeuSerArgLeuPheAspAsnAlaSer 40

122

21 63

41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe-----

CTCCCCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGAAGAAGCC

-----AsnProGlnThrSerLeuCysPhe 65

242 57 1 MetAlaThrGlySerArgThrSerLeuLeuLeuAlaPheGlyLeuLeuCysLeuProTrp

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                                                                                                                            US-09-856-796B-2 (1-202) x US-09-949-016-2780 (1-821)
                                                                                                                                                                                    Query Match:
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US-09-949-016-2780
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                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 2280
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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                    21 LeuGlnGluGlySerAlaPheProThrileProLeuSerArgleuPheAspAsnAlaSer 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAGAGTCTATTCCGACACCCTCCAACAGGGAGAAAACACAACAGAAATCCAACCTAGAG
                                                                                                 1 MetalaThrGlySerArgThrSerLeuLeuLeuLeuAlaPheGlyLeuLeuCysLeuProTrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC
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COMMENT PRILICATION INSIGNE 18(79)999-015
COMMENT FILLING DATE: 2000-0417.
PRICOR PRILICATION INSIGNE: 80741,755
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NEPLICANT, VENTER, J. CCAÍG EC AI.
TITLE OF INVESTICAN POLYARENISME IN KNOWN GENES ASSOCIATED
TITLE OF INVESTICAN: MITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF
TILS RETERBENCE: CLOGAISO'
                                                                                                                                                                                                                                                                                                                      ORGANISM: Human
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                      2.15e-114
996.00
92.17%
92.17%
95.13%
                              Matches:
Conservative:
Mismatches:
Indels:
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1 MetalaThrGlySerArgThrSerLeuLeuLeuAlaPheGlyLeuLeuCysLeuProTrp 20

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OGREBAL INFORMATION.

APPLICAMY TOWARDS J. CIALS et al.

APPLICAMY TOWARDS J. CIALS et al.

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; TYPE: DNA
; ORGANISM: Human
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APTLICANT: NUTRE, J. Craig et al.

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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
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CTTCANGAGGGCAGTGCCTTCCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTATG 182 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnAlaSer 40 MetAlaThrGlySerArgThrSerreuLeuLeuAlaPheGlyLeuLeuCysLeuProTrp

CTCCGCGCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGAAGAAGCC 24: LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe----- 57

-AsnProGlnThrSerLeuCysPhe 65

LeuLeuArgIleSerLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg TCAGAGTCTATTCCGACACCCTCCAACAGGGGGAAACACAAAAATCCAACCTAGAG SerGluSerIleProThrProSerAsnArgGluGluThrGlnGlnLysSerAsnLeuGlu 85 362

AGRETETTEGECAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 125 crecrecearerecrecrecrearecaderecreases acceeded and recrease 482 422 10

ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC ThrGlyGlnIlePheLysGlnThrTyrSerLysPheAspThrAsnSerHisAsnAspAsp -CTGGANGATGGCAGCCCCCGG 600 165 540

186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe

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                                                                                       rHisAsnAspAspAlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPhcArgLysAspMe 181
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WS-08-187-756C-1

Sequence 1. Application US/06187756C Patent No. 5597709
GENERAL INFORMATION THE APPLICANT: ROSEN, ET AL.
TITLE OF INVENTION: Human Growth Hormone NUMBER OF SEQUENCES: 7

CORRESPONENCE ADDRESS;
ADDRESSEE: CRECHI, STEMAT & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
SPATE: NOW LURSEY
SPATE: NOW LURSEY

ZIP: 07068

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ATTORNEY/ACENT INFORMATION:
NAME: FERRARO, GRECORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-55
TELEODAMUNICATION INFORMATION:
TELEPHONE: 201-994-1700

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-710-324A-1
                                                                                                                                         Sequence 1, Application US/08710324A
Patent No. 5962411
GENERAL INFORMATION:

APPLICANT: ..ROSEN, et al.

TITLE OF INVENTION: . Human Growth Factor
NUMBER OF SEQUENCES: 7
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CORRESPONDENCE ADDRESS:

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US-09-856-796B-2 (1-202) x US-08-710-324A-1 (1-654)
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPENTING SYSTEM: PC-DOS/NS-DOS
OPERATING SYSTEM: PC-DOS/NS-DOS
OPERATING SYSTEM: ARCHAEM #1.0.
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
NAME: Brockes, A. Anders
REGISTRATION NUMBER: 36,373
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/187,756
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TYPE: nucleic acid
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126 LysaspleuGluGluGlyIjeGlnThrLsuMetGlyArgLsuGluAspGlySsrProArg 145
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Gaps:
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Mismatches:
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greater tha greater tha greater t Query A7 100.0 1.5 98.3 1.5 98.3 1.5 98.3	N. Gene 1: 9e 2: 9e 3: 9e 4: 9e 5: 9e 6: 9e 6: 9e 7: 9e 9: 9e 10: 9e 11: 9e 11: 9e 11: 9e	ine parameters ine parameters 1/USPTO spool h teseq 15 bc04 - 7 0 - UNITS-bits - DOCALION-200 - L- OUTPM-pto 9855796 @CGN 1 -LARGEQUERY - NE OUT-120 - WARN T 7 - YGAPOP=10 - Y	g: Minimum Maximum Listing			: BLOSUM6 Xgapop Ygapop Fgapop Delop	118	Pebruary	nucleic	CO
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necon of the result beinage a decommendation. Printed, ord sorted distribution. Description Assets DNA encod Assets DNA encod Assets DNA encod Assets DNA encod Assets DNA encod Assets DNA encod Assets DNA encod Assets DNA encod Assets DNA encod Assets DNA encod Assets DNA encod Assets DNA encod Assets DNA encod Assets DNA encod Assets DNA encod Assets DNA encod Assets DNA encod Assets DNA encod Assets DNA encod		092205 12441 2551/app.guery.fasta_1.391 rg _41504705-5_1 _1.0026_0_0 RIZABJORNES_TRANS-himma40.cdi RIZABJORNES_TRANS-BANGO00000 \$50_0401_2551_4000_00000 \$51_24441_2551_400000000 \$51_24441_2551_4000000000 \$51_24441_2551_400000000000000000000000000000000000		Darameters: 8780412	residues		·····KVETFLRIVQCRSVEGSCGF 202	, Search time 532 Seconds (without alignments) 2247.721 Million cell updates/sec	frame_plus_p2n model	n 5.1.6 Compugen Ltd.

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ALIGNMENTS		Andrian Common Com	Add 8484 Himan	Manual Selection	Manager of the contract of the	Direction of the country of the coun	arataba.	Add 104 of 104 o	9 Adriado numan i	a force of	Adaga 7 Human	7 Adapte Human c	Adiaou/2 Human c	Adp43297 Human	Adp43293 Human	Adq38467 Human	Adq38456		Aan81286	Aav60639	Aan71239	Aan60678 S	Abx14644	Adn49719 Human	Acc78890 Humar	Aac86395 Human		Aa146250	TANGE OF THE PARTY		May33629	Aagus 700	Adiabay Human c	Adp19728	Adj93049 Human	Acc58425	Adc61349 Hum		

RRSULT 1 AAA46696 ID AAA46696 standard; DNA; 609 BP. XX

AAA46696;

25-SEP-2000 (first entry)

DNA encoding a human growth hormone (hgH).

Rhman; growth hormon; höd; inhibitor; nuclear factor-kappaB; NF-kappaB; milti-fung resistance Seng; ahligunit henyy, molid tumouz; malignant blood disease; leukaemia; lymphoms; solid cancer; de

Homo sapiens.

W0200030587-A2. CDS Location/Qualifiers
1. .609
/*tag= a
/product= "growth hormone"

25-NOV-1998; 98FR-00014858 24-NOV-1999; 02-JUN-2000. 99WO-FR002897.

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US-09-856-796B-2 (1-202) x ANA46696 (1-609)
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Query Match:
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Detecting growth hormone variants (GHI), useful in screening patients growth hormone irregularities, comprises comparing the nucleotide sequence of a GHI gene from a test sample with that of a standard

Disclosure; Fig 6; 95pp; English sequence of the human GH1 Cooper DN (UYWA-) 12-MAY-2000; 14-JUL-2000; 14-MAY-2001; 2001WO-GB002126

Procter AM, 2000GB-00011459 2000EP-00306004

Gregory J, Millar DS. MEDICINE

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RESULT 2
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                                                                                                                                                                                                                                                             Growth hormone 1, Gil; osteopathic; gene therapy; protein therapy; sidely discrete protein recention; disabetes; obesity; infection; acromegaly; gigantism; sodium resention; water retention; metabolic syndroms; mod disorder; litep disorder; water retention; metabolic syndroms; mod disorder; litep disorder; growth hormone deficiency; drowth hormone dysfunction; familial growth hormone deficiency;
                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding growth hormone 1 gene (GH1), major isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-2002
                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                              short stature, pituitary storage defect; human; chromosome 17g23; ss
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/*tag= & /product= "GH1"
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88888888 Inheritance of movel lations; evaluation the effects of dif materious not be structure and function of the dwalends and devalengement of speid adaptomatic tests for inherited did difficiency. This sequence encodes the enjoy; lesform of human growth homomoment, (diff), locked on chromosome the endough of t

Sequence 654 BP; 150 A; 207 C; 160 G; 137 T; 0 U; 0 Other

Pred Query Match: Best Local Similarity: Percent Similarity No. Scores: 3.73e-108 1029.50 93.09* 93.09* 98.33% Conservative: Mismatches: Indels: Gaps: 150020

US-09-856-796B-2 (1-202) x AAS18887 (1-654)

LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnAlaSer MetAlaThrGlySerArgThrSerLeuLeuLeuAlaPheGlyLeuLeuCysLeuProTrp 40 60

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ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC 651

AMS18888 standard;

DNA; 654 BF

12-MAR-2002 (Ilrst entry)

XSXFXSX DNA encoding growth hormone 1 gene (GH1), E56G mutant

Growth hormone 1; Gil; osteopathic; gene therapy; protein therapy; diabetes; obesity; infection; accomeshly; gigantisms condum execution; water retention; metabolic syndrone, mod disorder; steep disorder; Growth hormone depituaction; densilial growth hormone deficiency; short stature; pituitary storage defect; human; mutant; ds.

Synthetic sapiens

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mutation replace(17. /*tag= b

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14-MAY-2001, 2001WO-GB002126

12-MAY-2000; 2000GB-00011459 14-JUL-2000; 2000EP-00306004

(UYWA-) UNIV WALES COLLEGE OF MEDICINE

Ŋ × Gregory J, Millar DS

WPI; 2002-089798/12

Detecting growth hormone variants (dH), useful in screening patient for growth hormone tregularities, comprises comparing the nucleotide sequence of a GHI gene from a test sample with that of a standard sequence of the human GHI.

Disclosure; Fig 7; 95pp; English

The invention described a method of electrical voltation in growth hormone (cd) (ed); and therefore of deprinction in an individual; The method comprises comparing the nucleoids sequence of GHI gene obtained from the variation (ed) variation. The method is the electrical variation (ed) variation, the standard is even electrical variation (ed) variation. The standard is even electrical variation for the variation of producing variating protein for treating growth hormone irregularities or producing variating protein for treating the variation of

Pred. No.: Sequence 654 BP; 148 Þ 207 C; 162 Ģ 137 T; ٥ g 0 Other:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrGlyGlnIlePheLysGlnThrTyrSerLysPheAspThrAsnSerHisAsnAspAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTIGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA
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TATATCCCAAAGGAACAGAAGTATTCATTCCTGCAGAACCCCAGACCTCCCTGTTTC

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CTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG LeuLeuArgIleSerLeuLeuLleGlnSerTrpLeuGluProValGlnPheLeuArg TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAACCTAGAG SerGluSerIleProThrProSerAsnArgGluGluThrGlnGlnLysSerAsnLeuGlu 85 밁 片 Ś

122 CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT

LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe-----LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnAlaSer MetAlaThrGlySerArgThrSerLeuLeuLeuAlaPheGlyLeuLeuCysLeuProTrp

57 40

CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGAAGAAGCC

AsnProGlnThrSerLeuCysPhe

303 65 241 62 ATGGCTACAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCCTGG

US-09-856-796B-2 (1-202) x ABK81192 (1-821)

Query Match: Best Local Similarity: Percent Similarity: Pred. No.:

5.1e-108 1029.50 93.09 93.09 98.33

Conservative: Mismatches: Indels: Gaps: Length: Matches:

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14-NOV-2000;
09-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complex useful for transporting active agent through epithelal barrier, has biologically active portion and target cheant directed to ligand that confers e.g. transprotte properties to agent specific to ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Houston
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Sequence 821 BP;
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183 A, 270
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           196 G; 172 T;
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           0 U; 0 Other;
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                                                                                                                                                                                                                                 Sequence 3557 BP; 927 A; 902 C; 897 G; 831 T; 0
                                                                                                                                                                                                                                                           Sequence is derived from human pituitary gland tissue, and allows pro-
growth hormone to be produced by a circular plaemid carrying an amp
resistance gene, from a transformed E.o.jl expression system in an
ampiciliin containing medium. See also d51202590
                                                                                                                                                                                                                                                                                                                                                  Disclosure, Table 1-9; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                         Plasmid for amplification of human growth hormone gene - derived from human pituitary gland tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1986-276387/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAR-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAR-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NAKA/) NAKAJIMA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-SEP-1986.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human pro-growth hormone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAN60801 standard; DNA; 3557 BP
| MecAlaThr01/SerAsyThrSerInstealcusAlaPhe01/YeuLeuCysLeuProTrp 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      662 ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     602 GCACTACTCAMGAACTACGGGCTGCTCTACTGCTTCAGGAMGGACATGGACAAGGTCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 AleLeuLeuLysAsnTyrGlYLeuLeuTyrCysPheArgLysAspMetAspLysValGlu 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   542 ACTOGGCAGATCTTCHAGCHGACCTACHGCHAGTTCGACAAACTCACACAACGATGAC 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146
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	4 TATATCCCAAAGGAACAGAAGTATTCATTCCTGCAGAACCCCCAGACCTCCCTC
6	6 SerGluSerlleProThrProSerAsnArgGluGluThrGlnGlnLysSerAsnLeuGlu
634	4 TCAGAGTCTATTCCGACACCCTCCAACAGGGGAGGAAACAGAACAGAAATCCAACCTAGAG
86	6 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg
694	4 CIGCTCCGCATCTCCCTGCTGATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG
106	6 SerValPheAlaAsmSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu
754	AGTGTCTTCGCCAACAGCCTGGTGTACGGGGCCTCTGACAGCAACGTCTATGACCTCCTA 81
126	LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg
814	814 AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCCGG 873
146	
874	ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACACGATGAC 933
166	
934	GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGA
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994	ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGCCAGCTGTGGCTTC 1044
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ABK90830 standard; DNA; 654 BP

ABK9 RESU

ABK90830,

05-NOV-2002 (first entry)

Riman; growth hormone; hGH; Turner's syndrome; achondroplasia; growth hormone deficiency in adults; GHDA; chronic remai innufficiency; remai failure in children; acquired immune deficiency syndrome; AIDS; Masting; cachexia; gene; de. DNA encoding human growth hormone (hgH)

впатава опон

mat_peptide sig_peptide /*tag= b /product= 81..651 /*tag= Location/Qualifiers .654 "Human growth hormone"

SG

/*tag= c /note= "Mature human growth hormone"

WO200255532-A2

10-JAN-2002; 2002WO-DK000017. 18-JUL-2002

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US-09-856-796B-2 (1-202) x ABK90830 (1-654)
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11-JAN-2001; 2001US-0261411P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New conjugates exhibiting growth hormone activity, useful for treating disease or for manufacturing a medicament for treating a disease. e.g. Turner's syndrome, growth hormone deficiency, achondroplasia, AIDS wasting or cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 654 BP; 150 A; 207 C; 160 G; 137 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to new conjugates,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Page 73-74; 74pp; English
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                                                                                                                                                            LeuLeuArgIleSerLeuLeuLeulleGlnSerTrpLeuGluProValGlnPheLeuArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCCGCGCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGAAGAAGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe-----
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    AsnProGlnThrSerLeuCysPhe 65

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ADC61349 standard; DNA; 654
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A present invention valies to a method for descriping a variation in pitulary-expenses describ homeone (GRI) effective to est a am children comparator themsone (GRI) effective to est a am children comparator the beamson (GRI) effective to next simple with a translation comparator the beamson (GRI) effects the present sequence is the continuous expenses for human (GRI) used for illustrate, the method pass of the method pass of the continuous expenses of the continuous expenses of the continuous expenses of the continuous expenses of the four paraticipant store (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) content (CRI) cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; ADC61299
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/product= "Human growth hormone,
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                                                                                                                                                                       Growth hormone; GHI gene; human; cytostatic; antidiabetic; anorectic; antimicrobial; cardiant; gene therapy; chromosome 17q_i single nucleotide polymorphism; gene; ss.
                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                               Human growth hormone GH1 gene coding sequence
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P-PSDB; ABR42662 WPI; 2003-449559/42 Cooper DN, Procter AM, Gregory J, Millar DS, Lewis M, Ulied A,

Disclosure, Fig 5, 62pp, English. New polynucleotide comprising a variant of the human growth hormone mucleic acid ecquence, GHI, useful for diagnosing or treating obsetty, diabetes, infection, cancer or cardiac conditions.

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membrane barrier; human growth hormone.
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ADP19728 standard,

CDNA; 654 BP

ADP19728;

Human growth hormone 1 (GH1) encoding cDNA

(first

entry)

human; growth hormone; growth hormone veriant; GB; GBI; receptor-mediated cell signifies perhapy activator; growth hormone dywilmeticn; growth hormone irregularity; chromomome 17; 88.

Homo sapiens Location/Qualifier

.654

"growth hormone 1 (GH1)"

/*tag= a /product=

WO2004044002-A1

DB:

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RESULT 11 AAL46249

AAL46249 standard; DNA; 769 BP.

15-AUG-2002 AAL46249; (first entry)

Human growth hormone coding sequence SEQ ID NO: 29.

Wouse, human; natmal model; growth deficiency; cognitive function; growth hormone; IGP-1; enterporonie; eardiovascular disorder; dwarfism; illig-type deficiency; Kowarsby syndrome; dlabetes; accomegaly; gigantism; glomeruloscierosis; mutant; gene; de.

Homo sapiens.

WO200172119-A2.

02-APR-2001; 2001WO-EP003733. 04-OCT-2001.

31-MAR-2000, 2000DE-01016083.

(INGE-) INGENIUM PHARM AG.

US-09-856-796B-2 (1-202) x ADP19728 (1-654)

Cornali E, Nehls MC, Schlueter V, Wattler F, Wattler S, Wolf S;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page ?; -pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9005185-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 814 BP; 193 A; 259 C; 192 G; 170 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          656 ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC 706
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                                                                                                         100
                                                                                                                                                   21 LeuGlnGluGlySerAlapheProThrIleProLeuSerArgLeuPheAspAsnAlaSer 40
                                                                                                                                                                                                        40 ATGGCTACAGGCTCCCGGACGTCCCTGCTTTTGGCCTGCTCTGCCTTGG
                                                                                                                                                                                                                                                            1 MetalaThrGlySerArgThrSerLeuLeuLeuAlapheGlyLeuLeuCysLeuProTrp
                                               LeuhrghlaHisArgLeuHisGlnLeuhlaPheAspThrTyrGlnGluPhe-----
                                                                                                         CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAAGGCTATG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lecomte C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hormone; hGH; hypophysial; dwarfism; insulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88PR-00014514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88FR-00014514.
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40..690
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1024.50
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92.63%
97.85%
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Indels:
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gene having three vames a novel method for directing entragementy of a gene having three vames a fewerest as a directionally and spatially ordered feshion to produce a gene or a gene vector. The method involves	2) Page 107-110, 141pp; English	ing class IIS res			NATUR	1997;	FEB-1998; 98WO-		W09838326-A1.	Synthetic,		GENSA 981, a monomeric DNA sequence produced by the invention.	29-DEC-1998 (first entry)	AAV33629;		640 ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTT 690	98	580 GCACTACTCAAGAACTACTCACTACTCACTACTCACTACTCAAGAACTACTAAACTAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAAACTAAAAAA		146 ThrGlyGlnilePheLysGlnThrTyrSerLysePheAspThrAsnSerHisAsnAspAsp 165	460 AAGGACCTAGAAGGAAGCATCCANACCCTGATGGGGACTGGAAGATGGAACCACCCCCCCCCC	8		86 LeuLeuArgIleSerLeuLeuLeuIleGinSerTrpLeuGinDroValGinPhoLeuArg 10s	** SerčilleroffirProSerAsnArgGluGluThrGlnGlnLysSerAsnLeuGlu 85		160 CTCCGCGCCCCATCGTCTGCACCACCTGCCCTTTGACACCTACCAGGAGTTTGAAGGAAG
Db RESULT	S	8 8	₽	Ś	밁	Ş	D	Ś	Db	Ş	8 8 8	. 5	, B	્ર	B 5	, B	S	US-0	Quer DB:	Perc	Alic	8 X 8				: .	

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recognition sites, for industrial of the frequency expension and the decisions of the frequency expension of the frequency expension of the frequency expension of the frequency expension of the definition of the frequency expension of th
sequences from a cell, including those for enhanced biological action tissue-specific, hormone-specific or developmental-specific gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               containing class IIS restriction endonuclease
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Sequence 5594 BP; 1232 A; 1519 C; 1518 G; 1325 T; 0 U; 0 Other;

st Local Similarity: ed. No.: ry Match: Cent Similarity: No.: 2.72e-106 1024.50 92.63* 92.63* 97.85* Gaps: Mismatches: Matches: Conservative: Indels:

09-856-796B-2 (1-202) x AAV33629 (1-5594) 2330 CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTATG 2389 2270 Anddethachddereceddalogreechderechdaethiniadechderechdecethda 2325 21 LeuGlnGluGlySerAlaPherroThrIleProLeuSerArgLeuPheAspAsnAlaSer 40 1 MetAlaThrGlySerArgThrSerLeuLeuLeuAlaPheGlyLeuLeuCysLeuProTrp 20

41 IAUNSPALAHERANDES EITHEAN ARDENDETTYT GIRCLUPRE ------- 57

8 AsnProGlnThrSerLeuCysPhe 65

2570 CTGCTCCGCATCTCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG LeuLeuArglieSerieuLeuLeulleGinSerTrpLeuGluProValGinPheLeuArg 105 2629

2690 126 ANGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG LysAspLeuGluGluGlyI1eGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 2749

ThrolydinilePhoLysGlnThrTyrSorLysPhoAspThrAsnSorHisAsnAspAsp

8 8 8 8 8 8 8 8 8 8

2750 ACTOGGCAGATOTTCAAGCAGACCTACAOCAAGTTCGACACAAACTCACACAACGATGAC 186 166 AlaieuieuiysaanTyrGlyLeuLeuTyrCysPhoArgLysAspMctAspLysValGlu

2869 185 2809 165

2870 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202 ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC 2920

8 RESULT: 14

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AAV33621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                          US-09-856-796B-2 (1-202) x AAV33621 (1-7080)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV33621 standard; DNA; 7080 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class IIS restriction endonuclease recognition site;
endogenous mouse promoter element; tissue-specific gene expression;
bormone-specific gene expression; ss;
developmental-specific gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pVLOVhGH-900 DNA sequence used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 89-92; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          containing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7080 BP; 1691 A; 1813 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene expression
41 LeuargalaHisargLeuHisGlnLeualaPheAspThrTyrGlnGluPhe-----
                                                                                              2908 CTTCAAGAGGGCAGTGCCTTCCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTATG 296
                                                                                                                                                                                                                                       2848 Artoscracassácirocosaaceriocoriscrecióscritirosceriocireriocerioscerios 2907
                                                                                                                                                        21: LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnAlaSer 40
                                                                                                                                                                                                                                                                                                         MetalaThrGlySerArgThrSerLeuLeuLeuAlaPheGlyLeuLeuCysLeuProTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          assembling gene or gene vector - comprises use of primers class IIS restriction endonuclease recognition sites.
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Indels:
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ADM32918
                                                                                                         ADM32918 standard; cDNA; 654
                                     17-JUN-2004
                                                                           ADM32918;
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                                                                                                                                                                                     3448
                                                                                                                                                                                                                       186
                                                                                                                                                                                                                                                                                                                                                                   146 ThrGlyGlnIlePheLysGlnThrTyrSerLysPheAspThrAsnSerHisAsnAspAsp 165
                                                                                                                                                                                                                                                                                                                                                                                                                                           126 LysaspleuGluGluGlyTleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 145
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                                                                                                                                                                                                                                                                                           166 AlaLeuLeuLysaanTyrGlyLeuLeuTyrCyspheArgLysaspMoctAspLysValGlu 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA 3267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuLeuArgIleSerLeuLeuLeulleGlnSerTrpLeuGluProValGlnPheLeuArg
                                                                                                                                                                                     ACATTOCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC 3498
                                                                                                                                                                                                                                                             ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202
sequence of human growth hormone (hGH) protein
                                         (first entry)
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3447

88; hGH synonymous Nucleotide codon; translation efficiency; human; growth hormone; gene;

Homo gapiens

Gey Location/Qualifiers /product= "growth hormone .654

WO2004024915-A1

15-SEP-2003; 2003WO-AU001200. 25-MAR-2004

2002US-0410410P

(UYQU) UNIV QUBENSLAND 13-SEP-2002;

WPI, 2004-270043/25. Frazer IH;

P-PSDB; ADM32919.

Constructing a synthetic polymuclactide, useful for producing a spolypoptide at a higher lared in a more an overveil, comprises selecting a first codon of the parent polymuclactide for replacement with

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synonymous codon
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Example 3; Fig 3; 82pp; English

The specification describes a mainded day constructing a symitetic polymonia that from which a polymonia day constructing a syminal to the united seems in a Chinese America Oray, (CRO) call compared to when united as salecting a time code on other than the same polymonia. The method comprises a personal codes, where the promonous codes is not created a censult with the late first codes of the symmetry codes is not created a censult with the late first codes of the code

Sequence 654 BP; 150 A; 208 C; 160 G; 136 T; 0 U; 0 Other;

Alignment Scores: Score Pred. No.

DB: Percent Similarity: Best Local Similarity: Query Match: 8.83e-107 1017.50 92.17% 92.17% 92.17% 97.18% Conservative: Mismatches: Matches: Indels:

US-09-856-796B-2 (1-202) x ADM32918 (1-654)

21 LeuGlnGluGlySerAlaPheProThrileProLeuSerArgLeuPheAspAsnAlaSer 40 MetAlaThrGlySerArgThrSerLeuLeuLeuAlaPheGlyLeuLeuCyeLeuEroTxp 20

121 41 CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGAAGAAGCC 180 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe------57 CTTCANGAGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCCTTTTGACAAGGCTATG 120

61

98

361 106 301 SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLou 12s CTGCTCCGCATCTCCCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA 420 360

LeuLeuArgIleSerLeuLeuLeuIleGinSerTrpLeuGluProValGinPheLeuArg 105

601 186

ThrPheLeuArg1leValGlnCymArgSerValGluGlySerCysGlyPhe 202

600

Search completed: Pebruary 7, 2005, 13:48:06 Job time: 539 secs

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ALIGNMENTS

RESULT 1 BD270127 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM
B270127 B270129 B activation inhibitors and their wess as drug. B8701274. C:13079895 UP 200527224-A/A. unidentified unidentified

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REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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Location/Qualifiers	B activation inhibitors	Topology: Linear;	Strandedness: Double;	C07K14/505, C07K14/52, C07K14/61 C15N1E/00	A61P35/00//	A61K45/00, A61K31/337, A61K31/475 A61K31/6	FRANCOIS HIRSCH, ASTRID HARFFNER	-1998 FR	24-NOV-1999 JP 2000583472	05-NOV-2002	JP 2002537224-A/1	Unidentified

9,A61K37/02,C12N15/00 55,A61K38/00,A61K45/06,

Topology: Linear; NF-Kappa B activation inhibitors and their uses as drug FH Location/Qualifiers

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sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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DEFINITION BC062475

ACCESSION BC062475 BC062475.1 GI:38566151 277 bp mRNA linear PRI 30 BOOGE475 Homo sapiens growth hormone 1, transcript variant 2, mRNA clone MGC:75439 IMAGE:30393581), complete cds.

KEYWORDS SOURCE ORGANISM Homo sapiens (human) Homo sapiens

REPERBNCE AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Strumberg R. I., Patagod E. N., Grosse L. I., Begrad G. M., Schlars G. D. Allamer, S. D., Collins F. S., Wagner L., Blemenn C. W., Schlars G. D. Allamer, S. D., Collins F. S., Wagner L., Blemenn C. W., Schlars G. D. Hardwick, S. G. S., Wagner L., Blemenn C. W., Schlars G. D. Hardwig S. B. Hardwick, S. G. S., Schlars G. D., Hardwig S. B. Hardwick, S. G. S., Schlars

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PUBMED REFERENCE AUTHORS TITLE

(bases 1 to 777)

JOURNAL STILL

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Duano Smailus, Jeff Stort, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                    342. GTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTAGGGCGCCTCTGACAGCAAC
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                                                                                                                                                                                                                                                                                                                  AshProGlnThrSerLeuCysPhe 65
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Db	g	US-09-8	Alignment pred. No. Score: Secret S Best Loca Query Mat DB:	JOURNAL FEATURES SOUL	REFERENCE AUTHORS TITLE	VERSION KEYWORDS SOURCE ORGANISM	RESULT 5 AX300799 LOCUS DEFINITION ACCESSION	Dβ	Ş	8 1	δ <u>ε</u>	8	D)	δ	₽
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Location/Qualifiers
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Meurice outgrowth-promoting factor homologue and nucleic acids
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Mammalia; Butheria; Primaces; Catarrhini; Hominidas; Homo.
CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGAAGAAGCC 230
                                                        LeuArgAlaHisArgLeuHisGlnLeuAlsPheAspThrTyrGlnGluPhe-----
                                                                                   CTTCAAGAGGGCAGTGCCTTCCCCAACCATTCCCCTTATCCAGGCTTTTTGACAACGCTAGT
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                                                                                                                             MetAlaThrQlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTrp
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Curagen Corporation (US)
Location/Qualifiers
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Neurite outgrowth-promoting factor homologue and nucleic acids
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Nakajima,K. and Nagai,J.

RECOMBINANT PLASKID OF ESCHERICHIA COLI

GROWTH HORMONE COMPLEMENTARY STRAND DNA
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                                                                                                                                                                                SEGERALSSONEFEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent: JP 1986202689-A 1 08-SEP-1986;
NAKAJIMA KUNIO
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other sequences, artificial sequences
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NAKAJIMA KUNIO, NAGAI JUN
C12N15/00//C12P21/02;
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Artificial sequence, Genes
JP 1986202689-A/1
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hypothetical: No;
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                             /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Sequence 3 from Patent W002055532.
AX481369
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                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                            Homo sapiens
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Growth hormone variations and their uses
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Salvado, J. Maria. Viader.
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NUMBER OF SEQ ID NOS: 66
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CURRENT APPLICATION NUMBER: US/09/853,688
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             PRIOR REPLICATION NUMBER: US 60/267,601
PRIOR PILLAR DATE: 2001-02-09
PRIOR REPLICATION NUMBER: US 60/248,819
PRIOR FILLAR DATE: 2000-11-14
PRIOR REPLICATION NUMBER: US 60/248,478
                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Publication No. US20030161809A1
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                                                                                                                         REPLICANT: BASU, AMARKEN TIONS AND METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVITIES OF INVESTION; COMPOSITIONS AND METHODS SEALULAN BARRIESS
TILE REFERENCE: 5072720-0501 SQ 507875, 748C
CHRESTO FILICO CHEET 2003-12-0705 CO1
CHRESTO FILICO CHEET 2003-12-0705 CO1
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PRIOR FILING DATE: 2000-11-13
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GREGORY, JOHN
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SHERIDAN, Philip, J.
HAWLEY, Stephen
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BASU, Amaresh
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US-09-969-748C-4
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LENGTH: 217
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PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 115
SOFTWARE: Patentin version 3.0
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Publication No. US20040137510A1
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/788,318
CURRENT FILMS DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 66
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TITLE OF INVENTION: HEFDON FOR DETECTING GROWTH HORMONE VARIATIONS IN TITLE OF INVENTION: LUDWANS, THE VARIATIONS AND THEIR USES
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APPLICANT: PROCTER, ANNIE
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                                               ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF
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pred. No. 1.1e-93;
0; Mismatches 0; Indels 15;
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Pred., No. 1.1e-93;
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US-09-929-918-9
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APPLICANT: KORdyum, Vitaliy A.
APPLICANT: Chernykh, Svitlana I.
APPLICANT: Slavchenko, Iryna Yu.
APPLICANT: Wozianov, Olaksandr
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
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                                          Matches 201;
                                                            Query Match
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Patent No. US20020090678A1
                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/929,918
CURRENT FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: 09/318,288
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ORGANISM: Homo sapiens
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APPALCANT GREGORY, CORE
TITLE OF STREET, ANNIE N.
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Publication No. US20040137510A1
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                              0; Mismatches
                                                      Score 1024.5; DB 9;
Pred. No. 3.5e-93;
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Pred. No. 1.1e-93;
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                                                                  APPLICANT:
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Publication No. US20040043446A1
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SEQ ID NO 16
APPLICANT: Chen, X1
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: ALPHA GALACTOSIDASE A:
TITLE OF INVENTION: GALACTOSIDASE A
TITLE OF INVENTION: GALACTOSIDASE A
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APPLICANT: CHEUNG, ANTHONY T.
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Zopf, David
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MATGSRTSLLLAFGLLCLPWLQEGSAFPTIPLSRLFDNASLRAHRLHQLAFDTYQEF---

57

CURRENT APPLICATION NUMBER: US/10/411,037

REFERENCE: 040853-01-5082

REMODELING AND GLYCOCONJUGATION OF ALPHA

165 120

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Sequence 16, Application US/09804409A
Patent No. US20020155100A1
                                                                                                                                                                                                                                                                              TITLE OF INVENTION: COMPOSITIONS AND METHOU
TITLE OF INVENTION: EXPERSION IN GUT
FILE REFERENCE: 02996/027 8721
CURRENT APPLICATION (NUMBER: US/09/804,409A
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ 1D NOS: 181-03-12
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                                Score 1017.5; DB 9; Length 217;
Pred. No. 1.7e-92;
     Mismatches
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2; Indels 15; Gaps

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; ORGANISM: Homo sapiens
US-10-411-037-48
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Publication No. US20040063911A1
GENERAL INFORMATION:
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LENGTH: 217
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PRIOR FILING DATE: 2002-08-28
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PRIOR REPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
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PRIOR FILING DATE: 2002-06-07
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PRIOR APPLICATION WINDER: US 60/344.692
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TITLE AS PREMICE: 00083-01-5053
THE REFERENCE: 00083-01-5053
CERRENT APPLICATIONS MODERS: UNIQUE 10083
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APPLICATION NUMBER: US 60/407,527
                                                                 FILING DATE: 2002-06-25
APPLICATION NUMBER: US 60/396,594
FILING DATE: 2002-07-17
APPLICATION NUMBER: US 60/404,249
                                       FILING DATE: 2002-08-16
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pred, No. 1.7e-92;
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US-10-410-962-48
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NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version 3.2
SEQ ID NO 48
                                                                                                                                                                                      , ORGANISM: Homo sapiens
US-10-410-962-48
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                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.2
SEQ ID NO 48
LENGTH: 217
                                                          Query Match
Best Local Similarity
Matches 200; Conserv
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CURRENT FILING DATE: 2003-04-09
RRIOR APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND TITLE OF INVENTION: GLYCOCOMJUGATION OF G-CSF
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PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
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PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/396,594
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PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
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Bowe, Caryn
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Zopf, David
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No. US20040077836A1
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Hakes, David
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                                                                       Score 1017.5; DB 15; Length 217;
Pred. No. 1.7e-92;
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PRIOS APPLICATION NAMES: US 60/344,592
PRIOS PILING DATE, 2001.0-6
PRIOS PILING DATE, 2001.0-6
PRIOS PILING DATE, 2002.0-6-8
PRIOS PILING DATE, 2002.0-6-8
PRIOS PILING DATE, 2002.0-6-8
PRIOS PILING DATE, 2002.06-25
PRIOS PILING DATE, 2002.06-25
PRIOS PILING DATE, 2002.06-25
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PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
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CURRENT APPLICATION NUMBER: US/10/411,049
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
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                                166 ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF 202
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                                                                           121 SVFANSLÝÝGASDSNÝÝDLÍKOLEBGIQTLMGRLEDGSPRÍGGIFKGTÝSKFDTNSHNOD 180
                                                                                                                                                                            61 YIPKEQKYSFLQNÞÓTSLÓÞSÉSIÞTÞSNREBTQQKSNLELLKÍSLLLÍÐSNLEÞVOÐLR 120
                                                                                                                                                                                                                       58 ------MPQTSLCPSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLR 105
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                                                                                                                 SVFANSLYYGASDSNYVDLLKDLEEGIGTLAGRIEDGSBRTTQJIFKGTYSKEDTNSHNDD 165
                                                                                                                                                                                                                                                                                  MATGSKTSLLLAPGLLCLPWLQEGSAPPTIPLSKPFDXWLKAHKLHQLAPDTYQEPEEA
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Hakes, David
Chen, Xi
Bowe, Caryn
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No. US20040082026A1
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92.2%, Pred. No. 1.7e-92;
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COMMENTA PELCOTION NUMBER 191,01410, 30

REIGN BRILDEN DONE MODELS (191,0141), 30

REIGN BRILDEN DONE MODELS (191,014), 32

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REIGN BRILDEN DONES (191,014), 33

REIGN BRILDEN BROSSES (191,014), 37

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REIGN BROSSES (191,01
                                                                                                                           Sequence 48, Application US/10410997
Publication No. US20040126838A1
                                                                                                           GENERAL INFORMATION:
                                                                APPLICANT:
                                                                           APPLICANT: Neose Technologies,
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Best Local Similarity
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ORGANISM: Homo sapiens
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SOFTWARE: PatentIn version
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PRIOR FILING DATE: 2002-08-28
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                                                                                                                                                                                                                                                                             181 ALLKNYGLLYCFRKDMDKVBTFLRIVQCRSVEGSCGF 217
                                                                                                                                                                                                                                                                                                                  166 ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF 202
                                                                                                                                                                                                                                                                                                                                                                        121 SVFÁNSLYYGÁSDSNYYDLLKÖLEBGIGTLMGRLEDGSFRTGGÍFKGTYSKFDTNSHNDD
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Defrees, Shawn
Zopf, David
Bayer, Robert
                                                                                                                                                                                                                                                                                                                                                                                                              SVFANSLVYGASDSNVYDLLKDLEEGIQTIMGRLEDGSPRTGQIFXQTYSKFDTNSHNDD 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MATGERTSLILAFGLICLPWIQEGSAFPTIPLSRFFDNAMLRAHRLHQLAFDTYQEFEEA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bayer, Robert
Hakes, David
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                                                                           Inc.
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Pred. No. 1.7e-92;
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APPLICANT

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ORGANISM: Homo sapiens
US-10-410-997-48
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CURRENT FILING DATE: 2003-04-09
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TITLE OF INVENTION: PRINCIPLE OF THE REPRESENCE: 01653-01-5059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
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NUMBER OF SEQ ID NOS: 75
SOPTWARE: PatentIn version 3.2
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PRIOR FILING DATE: 2002-06-07
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Publication No. US20040132640A1
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                                                                 NEPICLONI: BOWN, CATYME GOODESTATION METHODS AND PROTEINS/REFILES PRODUCED BY THE TITLE OF INVESTION GONCOMESTATION METHODS AND PROTEINS/REFILE ARE PRODUCED BY METHODS IN THE ARE PRODUCED ON MARKETS 195 1/1/4/11.012

ORDERNY FILING DATE: 1001-04-09

FRICE PROJECTION DATE: 2001-10-10

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PRIOR APPLICATION NUMBER: US 60/387,292
                                        PRIOR FILING DATE: 2001-10-19
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FILING DATE: 2002-07-17
PAPLICATION NUMBER: US 60/404,249
PILING DATE: 2002-08-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WATGSRTSLLLAFGLLCLPWLOEGSAPPTIPLSRPPDKAMLRAHRLHQLAFDTYOEFEEA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALLKNYGLLYCPRKOMDKVETFLRIVQCRSVEGSCGF 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bayer, Robert
Hakes, David
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Zopf, David
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92.2%; Pred. No. 1.7e-92;
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US-10-411-012-48
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PRIOR PEPINCATION INSERT: US 60/356,554
PRIOR NEPLICOTION INDERS: US 60/365,554
PRIOR PELING NOTE: 2002-07-6
PRIOR PEPINCATION INSERT: US 60/404,249
PRIOR PEPINCATION INSERT: US 60/407,527
PRIOR PEPINCATION INSERT: US 60/407,527
PRIOR PEPINCATION INSERT: US 68-88
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US-10-287-994-48
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SEQ ID NO 48
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PRICE REPLICATION NUMBER: US 60/128-523
PRICE FILING AND 2001-10-10
PRICE FILING AND 2001-10-19
PRICE REPLICATION NUMBER: US 60/344, 692
PRICE FILING AND 2001-10-19
PRICE REPLICATION NUMBER: US 60/387, 292
PRICE REPLICATION NUMBER: US 60/387, 292
PRICE REPLICATION NUMBER: 2002-06-07
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Publication No. US20040137557A1
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                                                                                 NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.1
SEQ ID NO 48
LENGTH: 217
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APPLICANT: BAKES, DAVID
APPLICANT COMPANY REPORTING AND GLYCOCONGUNATION OF PERTIDES
TITLE OF INVESTIGATION OF PERFECTION OF PERTIDES
THE REPRESENCE OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERS
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PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
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PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YIPKEQKYSELQNÞÓTSLÓFSESÍÞTÞSNREETQQKSNLELLRÍSLLLÍQSWLEÞVQFLR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bayer, ...
Taye, Caryn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DeFrees, Shawn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inde1s 15; Gaps
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; ORGANISM: Homo sapiens US-10-287-994-48

Ouery Match
97.2%; Score 1017.5; DB 16; Length 217;
Best Local Similarity 92.2%; Prod. No. 1.7e-92;
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1 MATGSRTSLLARGLLCLEMI,QBGSAFPTIFLSRLFDNASLRAHRLHQLAFDTYQEF--- 57

166 ALLKNYGLLYGFRKDWDKVETFLRIVQCRSVEGSCGF 202

Job time : 133 secs Search completed: February 6, 2005, 13:17:03 This Page Blank (uspto)

	891.5 85.1 241 3 US-09-4	891.5 85.1 194 3 US-08-459-906-4 Sequence 4,	891.5 85.1 194 2 US-08-183-21 Sequence 1	4 US-09-462-941-1 Sequence 5,	891.5 85.1 191 3 US-09-465-461-1 Sequence 1,	909 86.8 176 3 US-08-990-774-1 Sequence 1,	909 86.8 176 3 US-08-990-774-2 Sequence 2,	914 87.3 176 3 US-08-791-728-2 Sequence	924.5 88.3 274 3 US-08-784-582-73 Sequence 73	95.4 198 4 US-09-411-657-5 Sequence 5	999 95.4 198 2 US-08-710-324A-5 Sequence 5.	95.4 198 1 115-08-187-7550 Sequence 4.	1016.5 97.1 217 4 US-08-710-324A-4 Sequence 4	97.1 217 1 US-08-187-756C-4 Segmence 4	1024.5 97.9 217 4 US-09-029-018-0 Sequence 1	97.9 217 3 US-08-759-628-11 Sequence 1	97.9 217 3 US-08-785-271-10 Sequence 1	97.9 217 3 US-08-784-582-10 Sequence 10,	3 1024.5 97.9 217 3 116_08_e88 22 Sequence 51, Appl	98.3 217 1 US-08-469-486-51	No. Score Match Length DB ID Description	Regul 7		Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	11		Post-processing: Minimum Match OW Moximum Match 100% Listing Einze 45 summaries	Maximum DB seq length: 0 Maximum DB seq length: 200000000	Total number of hits satisfying chosen parameters: 513545	Searched: 513545 seqs, 74649064 residues	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	L WATGERTSLILLAFGILCUPWKVETFIRIVQCRSVEGSCGF 202	core: 1			Run on: February 6, 2005, 12:55:48 ; Search time 43 Seconds	OM protein - protein search, using sw model	Copyright (c) 1993 - 2005 Compugen Ltd.	
Best Local Similarity 93.1%; Pre			US-08-469-486-51	TOPOLOGY: linear	TYPE: amino acid	: LENGTH: 217 amino acids	INFORMATION FOR SEQ ID NO: 51:	TELEX: 200154		J TELECOMMUNICATION INFORMATION:	REFERENCE/DOCKET NIMBER 062	BEGIETHAMIE T. Clark	ATTORNEY/AGENT INFORMATION:	FILING DATE: February 4 199	APPLICATION NAMES OF THE	CLASSIFICATION: 530	FILING DATE:	APPLICATION NUMBER : 15 (00 / 1	SOFTWARE: #1.25	OS/M	<pre># MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible</pre>	COMPUTER READABLE FORM:	, IR	STREET: 225 Franklin Street CITY: Boston STATE: Massachusetts	APELICANT: Thosperson, Hans C APELICANT: Bliet, Thor Las APELICANT: BEZEROIT, Michael TITLE OF INTENTION: Improved TITLE OF INTENTION: Proceins NUMBER OF SQUIENCES: 58 CORRESPONDENCE ADDRESS: 58	GENERAL INFORMATION:	RSSULT 1 US-08-469-486-51 ; Sequence 51, Application US/08469 ; Patent No. 5799281			9 191 3 8 168 6	871.5 83 867.5 82	878.5 83.9 400 4	84.1 177 2 84.1 177 4	880.5 84.1 177 1	84.5 401 4	888.5 84.9 197 4 888.5 84.9 197 4	888.5 84.9 197 4 888.5 84.9 197-4	.1 245 4	_

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equence 20, tent No. 542	App	equence	equence 6, A	equence 6, Appl	Apr	equence 8659, A	equence 8657, a	656,	equence 2, App	,

ALIGNMENTS

TRE 51, Application US/08469486 TRAL TUPOPMATTON:
PLICANT: Thoegersen, Hans Christian PLICANT: Holtet, Thor Las
NVRNTION Michael
TLE OF INVENTION: proteins
: 225
otto
STATE: Massachusetts
켢
ZIP: 02110-2804
OMPUTER: TRM DC Compatible
ro.
OFTWARE: #1.25
RENT APPLICATION DATA:
TLING DATE:
OR APPLICATION DATA:
PPLICATION NUMBER: 08/192,060
AME: Paul T. Clark
30,1
ECOMMUNICATION INFORMATION:
BLEFAX: 617 542 8906
ELEX: 200154
ATION FOR SEQ ID NO: 51:
CS:
122
TRANDEDNESS:
POLOGY: linear
COLE TYPE: protein

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US-08-469-658-51
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GRNEPAT THE PATENT NO. 5917018
                                                                                               US-08-469-658-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Th egersen, Hans
APPLICANT: Holtet, Thor Las
APPLICANT: Etzerodt, Michae
                                Matches
                                              Query Match
Best Local Similarity 93.1%; Pred. No. 1.9
                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: IMPROVED
TITLE OF INVENTION: PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER OF SEQUENCES:
                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08
FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
FILING DATE: Februa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                STRANDEDNESS
                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                             TELEPHONE: 617 542 8906
                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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                                202; Conservative
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1 MATGSRTSLLLAFGLLCLPWLQEGSAFPTIPLSRLFDNASLRAHRLHQLAFDTYQEF--- 57
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                                                                                                                                                                                 217 amino acida
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                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                          February 4, 1994
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                                                                                                                                                                                                                                                                                                                                                                                              08/192,060
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                                    Pred. No. 1.9e-108;
0; Mismatches 0;
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                                          Indels 15; Gaps
                                                                        Length 217;
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                                                                                                                                                                                                                  US-08-589-028-10
                                                                                                                                                    Matches
                                                                                                                                                                                 Query Match
                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                 TELEPAX: (512) 474-757
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 217 amino acid
                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: UT
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 47,64.
                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Highlander, Steven L
                                                                                                                                                                                                                                      TOPOLOGY:
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No. 6087129mington, Karl D.
                                                                                                                                                                                                                                                                                    217 amino acids
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Quaade, Christian
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                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                  (512) 474-7577
                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                   (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fred
                                                                                                                                                                       97.9%;
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181 ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF 217
                                   166 ALLKNYGLLYGFRKDMDKVETFLRIVQCRSVEGSCGF 202
                                                                                               121 SVEANSLVYGASDSNÝYDLÍKOLEBÖJQTLMGRLEDGSPRTGQIFKQTYSKEDTNSHNOD 180
                                                                                                                                            106 SVEANSLYYGASDSNYYDLLKDLEEGIQTLMGRLEDGSPRTGQIFXQTYSKEDTNSHNDD 165
                                                                                                                                                                                              61 YIPKBOKYSFLQNPQTSLCFSSSIPTPSNREBTQQKSNLELLRISLLLIQSNLEPVQPLR 120
                                                                                                                                                                                                                                                58 -----NPQTSLCESESIPTESNREETQQKSNLELLRISLLLIQSWLEPVQFLR 105
                                                                                                                                                                                                                                                                                             MATGSRTSLLIAFGLLCLPWLOEGSAFFTFLSHLFUHASLAARLHQLAFDTYGSFEEA 60
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TITLE OF INVENTION: Recombinant Expression of Proteins From TITLE OF INVENTION: Secretory Cell Lines

Patentin Release #1.0, Version #1.30

Score 1024.5; DB 3; pred. No. 7.2e-108; 0; Mismatches 1; Length 217;

1 MATGSRTSILLARGLICIPWIQEGSARPTIPLSRLEDNASLRAHRLHQLARDTYQEF--- 57 Indels 15; Gaps

61 YIPKEQXYSFLQNÖQTSLCÖSESIÖTPSNREETQQKSNLELLRISILLIQSNLEEVQFIR MATGSRTSLLLAFGLLCLPWLQEGSAFPTIPLSRLFDNAMLKAHRLHQLAFDTYQEFEEA 60 NPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLR 105

120

166 ALLKNYGLLYCFRKDMDKVBTFLRIVQCRSVEGSCGF 202

121 SVFANSLYYGASDSNYYDLIADLEBGIQTIMGRIEDGSPRTGQTFKQTYSKEDTNSHNDD 180

106 SVFANSLVZGASDSNVZDLLKDLEEGTQTLMGRLEDGSPRTQIFKQTYSKFDTNSHNDD

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JS-08-784-582-10
                                                                                                                                      Query Match
Best Local
                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-784-582-10
                                                                                                                                                                                                                                                                   NFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 217 amino acids
                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: UT
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 6
FILING DATE: 15-OCT-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy
                                                                                                                                   Local Similarity
                                                                                                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MCGATTY, Dennis
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
TITLE OF INVENTION: SECRETORY CELL LINES
                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/589,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/784,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Arnold,
201,
                                                                MATGSRTSLLLARGLLCLDWLQEGSAFFITFLSRLEDNASLRAHRLHQLAFDTYQEF--- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10, Application US/08784582
o. 6110707
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                                             MATGSRTSLILLAFGLICLEMIQEGSAFFTIFLSRLFDNAMLRAHRLHQLAFDTYQEFEEA 60
                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Texas
                                                                                                                    Conservative
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                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                  512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 6110707mington, Karl D. Clark, Samuel A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Newgard, Christopher B.
Halban, Philippe A.
                                                                                                          97.9%; Score 1024.5; DB 3; 92.6%; Pred. No. 7.2e-108; tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Christian
                                                                                                                                                                                                                                                                                                                 37,642
UTSD:514
                                                                                                                                                                                                                                                                                                                                                                                                                                              US 60/028,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       White & Durkee
                                                                                                    Indels 15, Gaps
                                                                                                                                      Length 217;
                                                                                                                                                                                                      US-08-785-271-10
                                                                                                                                         Matches 201;
                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                      TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER NEADLABLE FORM:
MEDITAL TYPE: Ploppy disk
COMPUTER: 128 Competible
OPENATIAN SISTEM: PC-106/Mys_DG
SOFTMARE: Parentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                       TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19-JAN-1996
ATTORNEY AGENT INFORMATION:
Highlander, Steven L
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                     Local Similarity
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STRANDEDNESS:

217 amino acids

512/418-3000

REGISTRATION NUMBER:

37,642 US 08/589,028

UTSD:513

FILING DATE: Concurrently Herewith CLASSIFICATION: 435 APPLICATION NUMBER: US/08/785,271

APPLICATION NUMBER:

TOPOLOGY: linear TYPE: amino acid LENGTH:

Conservative

97.9%; Score 1024.5; DB 3; Length 217; 92.6%; Pred. No. 7.2e-108;

0; Mismatches

1, Indels 15, Gaps

MATOSRTSLLLAFGLLCLPMLQEGSAFFTPLSRLFDNAMLRAHRLHQLAFDTYQEFEEA 60 MATGSRTSLLLAFGLLCLPWLQEGSAFFTIPLSRLFDNASLRAHRLHQLAFDTYQEF--- 57

-----NPQTSLCFSESIPTPSNREETQQXSNLELLRISLLLIQSWLEPVQPLR 105

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US-08-785-271-10
GENERAL INFORMATION:
APPLICANT: Mesgard, Christopher B.
APPLICANT: Halban, Philippe A.
APPLICANT: No. 6194176mington, Karl D.
                                                                                                                        Patent No. 6194176
                                                                                                                                                                                                                                                 181 ALLKNYGLLYCFRKDMDKVSTFLRÍVÓCRSVÉGSCGF 217
                                                                                                                                                                                                                                                                                               166 ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF 202
                                                                                                                                   10, Application US/08785271
                                                                                                                                                                                                                                                                                                                                       121 SVFANSLVYGASDSNVYDLLKDLEBGIGTLMGRLEDGSFRTGGIFKGTVSKFDTNSHNDD 180
                                                                                                                                                                                                                                                                                                                                                                                     106 SVFANSLYYGASDSNYYDLLKDLEEGIGTLWGRLEDGSPRTGQIFKQTYSKFDTNSHNDD 165
                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLLIQSWLSPVQFLR 120
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APPLICANT: Thigpen, Anice E.
APPLICANT: Quade, Christian
APPLICANT: Kruse, Fred

RECOMBINANT EXPRESSION OF PROTEINS FROM

COUNTRY: USA CITY: Houston

Texas

77210

ADDRESSEE: Arnold, White & Durkee

P.O. Box 4433

APPLICANT:

Clark, Samuel A

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US-08-759-628-11
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Matches 201; Conservative
                             Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                 Best
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMIJAN PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                FEATURE:
                                                                                                                                                                            PEATURE
                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/008,574
FILING DATE: 06-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
              Local Similarity
                                                                                                                                                                                                                                                  NAMB/KEY:
                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                        OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                   LOCATION:
                                                                                                                    NAME/KEY:
                                                                                                                                                 LOCATION:
                                                                                                                                                             NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                                                                                                                                                                                                                                                                                                                   217 amino acids
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                                                                                                                                                                                       Peptide
94..115
                                                                                                                                              Peptide
133..153
                                                                                                        192..210
                                                                                                                                                                                                                                      32..53
                                                                                                                                                                                                                                                                                             linear
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                                                                                                                 Peptide
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                                                                                                                                                                                                                                                                                                         single
                       92.6%
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                                                                           /note= "The peptides above are
depicted in Figure 1"
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                       Score 1024.5; DB 3;
Pred. No. 7.2e-108;
           Mismatches
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              Indels 15; Gaps
                                        Length 217;
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1 MATGSRTSLLLAFGLLCLPWLQEGSAFPTIPLSRLFDNASLRAHRLHQLAFDTYQEF--- 57

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Patent No. 6342375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/284,878
CURRENT FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/MX37/00033
PRIOR FILING DATE: 1997-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SALVAGO,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Olazaran, Marcha Guerran
APPLICANT: Saldana, Hugo Barria Viader
APPLICANT: Salvado, Jose Maria Viader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEC ID NOS: 9
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            GENERAL INFORMATION: (LAILY A. APPLICANT ROCEPURA. SELILANA I. APPLICANT ROCEPURA. SELILANA I. APPLICANT ROCEPURA. SELILANA I. APPLICANT PAGE-DEFENDENT SUPER PRODUCTION OF TITLE OF INVESTION SELECTION FOR THE PROTEIN AND PER TITLE OF INVESTION SELECTION ACTUAL PAGE-DEFENDENT SUPER PRODUCTION OF TITLE SERVENCES. SELECTION SELECTION.
                                                                                                                                                                              Sequence 9, Application US/09929918
Patent No. 6773899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
CURRENT APPLICATION NUMBER: US/09/929,918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match
Local Similarity 92.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 SVEANGLYYGASDSNYYDLLKĎLEEGIGTLWGRLEDGSPRTGGIFXGTYSKFDTNSHNDD 165
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                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                        166 ALLKNYGLLYCFRKDMDKVSTFLRIVOCRSVEGSCGF 202
                                                                                                                                                                                                                                                                                                                                                                                     121 SVFANSLYYGASDSNYYDLLKDLEBGIQTLMGRLEDGSPRTGQIPKQTYSKPDTNSHNDD 180
                                                                                                                                                                                                                                                                                                                                                                                                                         106 SVENNSLVYGASDSNVYDLLKDLEBGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YIPKEQKYSFLQNPQTSLCPSESIPTPSNREETQQKSNLELLRISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MATGSRTSLLLARGLLCLPHIQEGSAFPTIPLSRLFDNASLRAHRLHQLAFPTYQEF--- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALLKNYGLLYCFRKOMDKVETFLRIVQCRSVEGSCGF 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MATGSRTSLLLAPGLICLPWLQBGSAPPTIPLSRLFDNAMLRAHRLHQLAPDTYQBFBEA 60
                                                                                                                                                                                                                                                                                                        ALLKNYGLLYCFRKOMDKVETFLRIVQCRSVEGSCGF 217
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.2e-108;
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                                                            PEPTIDES
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US-08-187-756C-4
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                                                            INFORMATION FOR SEQ ID NO. SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08187756C
Patent No. 5597709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                 REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/187,756C
FILING DATE: January 27, 1994
CLASSIFICATION: 43
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/318,288
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Human Growth Hormone NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                 STRANDEDNESS:
                                                     LENGTH:
                                                                                                                                                                      NAME: FERRARO, GREGORY
REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 SVFANSLYZGASDSNYYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHRDD 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YIPKEQKYSELQXÞÓTŠLÓFSESÍÞTÞSNREBTQQKSNLBLLRÍSLLLÍQSRLBÞVQFLR 120
                               AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 ------NPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MATGSRTSLLLARGLLCLPHLOEGSAPPTIPLSRLFDNASLRAHRLHQLAFDTYQEF--- 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MATGSRTSILLAPGILCIDMIGEGSAFPTIPLSRLPDNAMLRAHRLHQLAFDTYGEFEEA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROSEN, ET AL.
LINEAR
                                                                                                                                                                                                                                                                                                                                                                             IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.91;
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                                                                                                                                                 325800-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1024.5; DB 4;
Pred. No. 7.2e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 217,
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US-08-710-324A-4 Query Match Best Local Similarity Matches 200; Conserv

MOLECULE TYPE: PROTEIN

1 MATGSRYSLLLAPGILCLEWLOBGSAFFTIFLSRLFDNASLRAHRLHOLAFDTYGEF---

Conservative

97.14;

Score 1016.5; DB 2; Pred. No. 5.8e-107; 0; Mismatches 2;

Indels 15; Gaps

STRANDEDNESS TYPE: AMINO ACID

TOPOLOGY:

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 217 AMINO ACI

217 AMINO ACIDS

REFERENCE/DOCKET NUMBER: PF TELECOMMUNICATION INFORMATION: TELEPHONE: 301-309-8504

ATTORNEY/AGENT INFORMATION: CLASSIFICATION: 435 PRIOR APPLICATION DATA:

27-JAN-1994

US 08/187,756 36,373 PF104D1.SKB

NAME: Brookes, A. Anders REGISTRATION NUMBER: 36, APPLICATION NUMBER: FILING DATE: 27-JAN

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US-08-710-324A-4
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                                                                                                                                                                                                                                                                                                                                Atent No. 5962411

APPLICANT: Rosen, et al.

APPLICANT: Rosen, et al.

TITLE OF INVENTION: Human Growth Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 200; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
            MEDIDM TYPE: Floppy diak
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-COS/MS-DOS
OPERATING SYSTEM: PC-COS/MS-DOS
OPERATING SYSTEM: PC-COS/MS-DOS
OPERATINE: Patentin Railanse #1.0, VG
CURRENT APPLICATION NUMBER: US/08/710,324A
APPLICATION NUMBER: US/08/710,324A
                                                                                                                                                 COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                      COUNTRY: USA
ZIP: 20850
        FILING DATE:
                                                                                                                                                                                                                 STATE: MD
                                                                                                                                                                                                                                  CITY: Rockville
                                                                                                                                                                                                                                               ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 ALLKNYGLLYCFRKDMDKVETFLRIVOCKSVEGSCGF 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 SVFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 -----NPQTSLCFSESIPTPSNREETQQXSNLELLRISLLLIQSWLEPVQFLR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MATGSRTSLLLAFGLLCLPWLQEGSAFPTIPLSRLFDNASLRAHRLHQLAFDTYQEF--- 57
                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08710324A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAAGSKTSLULAPGLICLSWLQEGSAFPTIPLSKLFDNASLKAHKLHQLAFDTYQEFERA 60
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16-SEP-1996
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Pred. No. 5.8e-107;
0; Mismatches 2; Indels 15;
                                                           Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15,
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US-09-411-657-4
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US-09-411-657-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6566328
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                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 92.2%;
                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 217 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible operATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: P2-ECENTARE BECENTER BLOSS #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/411,657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,373
REPERENCE/DOCKET NUMBER: PF104D1.SKB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 ALLKNYGLLYCFRKOMDKVETFLRIVQCRSVEGSCGF 217
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                                                                                                                                                                                                                                200;
                                  106 SVEANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD 165
                                                                         61 YIPKEQKYSFLQNÞÓTSLCFSESIFTÞSNRESTQÓKSNLELLRÍSLLLÍÐSHLEÞVQFLR 120
                                                                                                            58 -----NPQTSLCFSESIPTPSNREETQQXSNLELLRISLLLIQSWLEPVQFLR 105
                                                                                                                                                  1 MAAGSRTSLLLAPGLICLSWLQEGSAFPTIPLSRLFDNASLRAHRLHQLAFDTYQEFEEA 60
                                                                                                                                                                                     1 MATGSETSLILLARGILCLPWLQEGSAFPTIPLSRLFDNASLRAHRLHQLAFDTYQEF--- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brookes, A. Anders
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                                                                                                                                                                                                                                                                                                                                                                                  AMINO ACID
SVFANSLYYGASDSNYYDLLKDLEEGIGTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD 180
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                                                                                                                                                                                                                                Score 1016.5; DB 4; Length 217;
pred. No. 5.8e-107;
0; Mismatches 2; Indels 15;
                                                                                                                                                                                                                                       Indels 15; Gaps
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                   US-08-710-324A-5
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                    177
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sequence 5, Applic
patent No. 5597709
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                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Human Growth Hormone
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/187
FILING DATE: January 27, 1994
                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ALLKNYGLLYCFRKOMDKVETFLRIVQCRSVEGSCGF 217
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                                                                                                                                                                                                                                                                                              196; Conservative
                              181 MDKVETFLRIVQCRSVEGSCGF 202
                                                                                                     121 VYDLIKOLBEGIQTIMGRIEDGSPRIGQIFKQTYSKFDINSHNDDALIKNYGILYCFRKD 180
                                                                                                                                           58 -SLCFSESIPTESKREETÖÖKSKLELLRISLLLIĞSKLEPVQFLRSVFAKSLVYGASDSN 116
                                                                                                                                                                             61 TSLCESESIPTESNREETQQKSNLELLRISULLIQSWLEEVQFLRSVFANSLVYGASDSN 120
                                                                                                                                                                                                                   1 MANGSRTSLLLARGLLCLSWLQEGSAFPTIPLSRLFDNASLRAHRLHQLAFDTYQEF--- 57
                                                                                                                                                                                                                                                         1 MATGSRTSLLLAFGLLCLPWLQEGSAFFTIBLSRLFDNASLRAHRLHQLAFDTYQEFNPQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08187756C
                                                                                                                                                                                                                                                                                                                                                                                                                                              4: 198 AMINO ACIDS
AMINO ACID
                                                                   VYDILKDIEEGIQTLWGRLEDGSPRTGQIFKQTYSKEDTNSHNDDALLKNYGLLYCERKD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 BECKER FARM ROAD
MDKVETFLRIVÇCRSVEGSCGF 198
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CECCHI, STEWART & OLSTEIN
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                                                                                                                                                                                                                                                                                                                 95.4%;
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                                                                                                                                                                                                                                                                                                                                    Score 999; DB 1;
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Gaps

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US-09-411-657-5
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                                                                                                                                Sequence 5, Application US/09411657
                                                                                                                          Patent No. 6566328
                                                                                       GENERAL INFORMATION:
APPLICANT: Rosen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
   CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                           NUMBER OF SEQUENCES:
                                                                              TITLE OF INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 5, Application US/08710324A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 27-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOPTWARE, Patentin Kell
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                        181 MDKVETFLRIVQCRSVEGSCGF 202
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                                                                                                                                                                                                                                                                                       121 VYDLIKDIEEGIQTIMGRIEDGSPRTQQIFKQTYSKFDTNSHNDDALLKNYGLLYCFRKD 180
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                                                                                       Rosen, et al.
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9410 Key West Avenue
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N'ENTION: Human Growth Factor
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                                                                     Human Growth Factor
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Pred. No. 4.9e-105;
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                                                                                                                                                                                                                                     Patent No. 6110707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                     APPLICANT: McGarry, Dennis
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
TITLE OF INVENTION: SECRETORY CELL LINES
                                                                                                    APPLICANT:
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LENGTH: 198 AMINO ACID
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                        INFORMATION:
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Quaade, Christian
Kruse, Fred
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TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTES: TEM PC *COMPATIBLE
OPERATING NOTES!
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NAM.
APPLICATION NUMBER: U8/09/411,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                   177 MDKVETFLRÍVÓCRSVEGSCGF 198
                                                                                                                                                                                                                                  181 MDKVETFLRIVQCRSVEGSCGF 202
                                                                                                                                                                                                                                                                    117 VYDLLKDLEBGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDDALLKNYGLLYCFRKD
                                                                                                                                                                                                                                                                                                       121 VYDLLKDLEEGIQTLAGRLEDGSPRTGQIFKQTYSKFDTNSHNDDALLKNYGLLYCFRXD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAAGSRTSLLLAFGLLCLSWIQEGSAFPTIFLSRLFDNASLRAHRLHQLAFDTYQEF--- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MATGSRTSLLLARGLLCLPWLQEGSAFFTIFLSRLFDNASLRAHRLHQLAFDTYQEFNPQ 60
                                                                                                           Application US/08784582
Clark, Samuel A
           Halban, Philippe A.
No. 6110707mington, Karl D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                 Christopher B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.0%; Pred. No. 4.9e-105;
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Houston

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COURTY: Tessa
COURTY: 108.
COURTY: 108.
COURTES: IMM FC COMPATIBLE
COMPATIBLE PROPY CLAR
COMPATIBLE IMM FC COMPATIBLE
COMPATIBLE IMM FC COMPATIBLE
COMPATIBLE COURTING DATA.
COMPATIBLE COURTING DATA.
APPLICATION NUMBER: UNFO. 1074-107.
FRICE APPLICATION NUMBER: US 6/020.477
APPLICATION NUMBER: US 6/020.477
APPLICATION NUMBER: US 6/020.477
APPLICATION NUMBER: US 6/020.477
APPLICATION NUMBER: US 6/020.477
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPHONE: 512/47-7577
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                  NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:514
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Query Match 88.5%; Score 926.5; DB 3; Length 360; Best Local Similarity 87.6%; Pred. No. 2e-96; Matches 7; Indels 15 181 ALLKNYGLLYCFRKDMDKWQRSLQDTEEKS 210 166 ALLKNYGLLYCFRKDMDKVETFLRIVQCRS 195 121 SVPANSLVYGASDSNYYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD 180 106 SVEANSLYVGASDSNYYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD 165 61 YIPKEQKYSFLONPOTSLCPSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQPLR 120 1 MATGGRTSLLLAPGLLCLPWLQEGGAPPTIPLSRLFDNASLRAHRLHGLAFDTYQEF--- 57 MATGSRTSLLLAFGLICLPMLQBGSAFFTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEA 60 15; Gaps

-08-784-582-73

TYPE: amino acid STRANDEDNESS:

LENGTH: 360 amino acids TOPOLOGY: linear

Search completed: February 6, 2005, 13:06:01 Job time : 44 secs

Run on: OM nucleic -

protein search, using frame_plus_n2p model

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd

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1028.5 1025.5 1025.5 1025.5

1 1047 94. 2 1042 93.7 3 1042 93.7 4 1095.5 92.6 5 1093.5 92.6 6 1093.5 92.6 7 1093.5 92.6 9 1093.5 92.6 9 1093.5 92.6 9 1093.5 92.6 9 1093.5 92.6	Result Query	Pred. No. is the score greater than and is derived	Database : 1	Command line parameters: -WDDELSTRAME, DDE model -Q-/-GDA_I/USFO good LD -Q-/-GDA_I/USFO good LD -BB-A_GGENERQ_ISEGGO LD -ISEG-A_GGENERQ_ISEGGO LD -ISEGGENERQ_ISEGGO LD -ISEGGENERQ_ISEGGO LD -ISEGGENERQ_ISEGGO LD -WDDE-LOCAL -OUTFWT=pto -WDDE-LO	.Post-processing: Min Max Lis	Minimum DB seq length: Maximum DB seq length:	Total number of hits	Searched: 2105692	Scoring table: BLOSUM Xgapop Ygapop Fgapop Delop	score: 1:	Run on: Feb
2002 2002 2002 2002 2002 2002 2007 2017 5 2017 5 2017 5	SUMMARIES	No. is the number of results preater than or equal to the greater than are equal to the to	Geneseq_16Dec04:* geneseqp1990s:* geneseqp1990s:* geneseqp2000s:* geneseqp2002s:* geneseqp2003bs:* geneseqp2003bs:*	p. modal . DRV-x1D p. modal . DR	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	h: 0 h: 2000000000	satisfying chosen parameters:	seqs, 386760381	BLOSUM62 Xgapop 10.0, Xgapext 0.5 Ygapop 10.0, Ygapext 0.5 Ygapop 6.0, Fgapext 7.0 Delop 6.0, Delext 7.0	US-09-856-796B-1 1112 1 atggctacaggctcccggac	February 6, 2005, 13:05:19
Apy93631 Ad38898 Ad38898 Au 6051 Au 11773 Au 11773 Au 11773 Au 11773 Au 11773 Au 11773 Au 11773 Au 11773		results predicted by chance to he to the score of the result besi of the total score distribution.		Command Line pharmeters: - MODILE-Crames. app. acad NEW-Alp - (-SDIZ_LINEFO, SDOOL_P)/NEO9385795/rman. o 60022005 124653 3477/app.quary. fan - (-SDIZ_LINEFO, SDOOL_P)/NEO9385795/rman. o 60022005 124653 3477/app.quary. fan - (-SDIZ_LINEFO, SDOOL_P)/NEO9385795/rman. o 60022005 124653 3477/app.quary. fan - (-SDIZ_LINEFO, SDIZ_LINEFO, SDIZ_L	.09		nrameters: 4211384	residues		agggcagctgtggcttctag 60s	:19 ; Search time 129.5 ; (without alignments) 3637.638 Million cell
Apy3637 Anino aci. Ade3938 Juman myo Ade3938 Juman myo Ade3938 Juman myo Ade3938 Juman myo Ade3938 Juman myo Ade3938 Juman myo Ade3938 Juman myo Ade3938 Juman myo Ade3938 Juman myo Ade3193 Growth ho Ade3193 Growth ho Ade3193 Growth ho Ade3193 Growth ho Ade3193 Growth ho Ade31943 Growth ho Ade31943 Juman gro		to have a being printed, ion.		ppp_query.fasta_1.775 DOPCI_0 human#0.cdi NAIGN=15 NAIGN=5 - ICPU-3 F= 0.5 - FGAROP=6						totag 609	Seconds

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Human	Aab49195	AAB49195	-	9	•
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	Adp19729	ADP19729	8	217	
Prote	Adq17923	ADG17923	7	217	-
	Adc61299	ADC61299		217	ш
Human	Aao29552	AA029552		217	-
Human	Abr42662	ABR42662		217	-
Protein	Aa019993	AA019993		217	_
Growth	Aau11721	AAU11721		217	-
Growth	Aau11740	AAU11740		217	-
	Aau11743	AAU11743		217	-
Growth	Aau11750	AAU11750		217	-
Growth	Aau11736	AAU11736		217	-
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Growth	Aau11727	AAU11727		217	-
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ALIGNMENTS

1024.5 1024.5 1024.5 1024.5 1024.5 1023.5 1023.5 1023.5 1023.5

AAY93637 standard; protein; 202 AA.

MY93637;

RESULT 1
AAY93637
ID AAY9
XX
AC AAY9
XX
AC AAY9
XX
AC JS-8;
XX
DF Amin
XX
Fumai Amino acid sequence of a human growth hormone (hGH). 25-SEP-2000 (first entry)

hlman; growth hormone, hdH; inhibitor; nucler factor-kappaB; NF-kappaB; mmltt-drug resistence gone; malignant hemopath; solid cunour; mmlignant blood disease; leukasmis; lymphoma; solid cancer.

Homo sapiens.

WO200030587-A2.

02-JUN-2000.

25-NOV-1998; 98FR-00014858. 24-NOV-1999; 99WO-FR002897.

(CNRS) CENT MAT RECH SCI.

Hirsch F, Haeffner A,

WPI; 2000-399901/34. N-PSDB; AAA46696.

Treatment of hematological or solid tumore using an inhibitor of the activation of nuclear factor-kapas particularly to prevent development of resistance to chemotherapeutics.

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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
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18-NOV-2004 (first entry)
                             ADQ39295;
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cardiant; gene therapy; human Human myocardial infarction-associated gene derived protein, SEQ ID 958 Myocardial infarction; detection; single nucleotide polymorphism; SNP;

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22-DEC-2003; 2003WO-US040978
                            15-JUL-2004.
                                                        WO2004058052-A2
                                                                                  Homo sapiens
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(APPL-) APPLERA CORP	20-DEC-2002; 10-MAR-2003; 30-APR-2003; 23-SEP-2003;
ERA CORP.	2002US-0434778P. 2003US-0453135P. 2003US-0466412P. 2003US-0504955P.

Cargill M. Devlin JJ, Iakoubova 0;

Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's mucleic secis.

The impact of the control and the control and the control and individual who compared the control and the cont Claim 10; SEQ ID NO 958; 145pp; English.

Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Dest Local Similarity: Query Match: DB:
3.35e-90 1042.00 99.50% 99.50% 93.71%
Length: Matches; Conservative: Mismatches: Indels: Gaps:
202 201 201 0

ADQ39295 ID ADQ: XX

ADQ39295 standard; protein; 202 AA

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US-09-856-796B-1 (1-609) x ADQ39295 (1-202)
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21 CTTCMAGAGGGASTGCCTTCCCAACANTCCCTTATCCAGGCTTTTTGACAACGCTAGT 120

41 CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTAACCCCAG LeuArgAlaHisArgLeuHisGinLeuAlaPheAspThrTyrGinGluPheAsnProGin 60

181

GTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCTGGTGTACGGCGCCCTCTGACAGCAAC LysSerAenLeuGluLeuLeuArgileSerLeuLeuLeuileGinSerTrpLeuGlubro

360

181 ATGGACAAGGTCGAGACATTCCTGCGGATCGTGGAGTGCCCTCTGTGGAGGGGAGCTGT MetAspLysValG luThrPheLeuArgIlevalGinCysArgSerValGluGlySerCys 200 600

ADQ39284

ADQ39284 standard, protein, 202

Human myocardial infarction-associated gene derived protein, 18-NOV-2004 (first entry)

Myocardial infarction, detection, single nucleotide polymorphism, SNP, therapy; human

Homo sapiens

W02004058052-A2

20-DEC-2002; 10-MAR-2003; 22-DEC-2003; ; 2002US-0434778P. ; 2003US-0453135P. ; 2003US-0466412P. ; 2003US-0504955P. 2003WO-US040978

(APPL-) APPLERA

Cargill M, Devlin JJ, Takoubova 0

Identifying an individual myocardial infarction by che individual's nucleic (acide l who has an altered risk for developing detecting a single nucleotide polymorphism

Claim 10; SEQ ID NO 947; 145pp; English

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US-09-856-796B-1 (1-609) x ADQ39284 (1-202)

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£ LeuArgAlaHisArgLeuHisG CTCCGCGCCGATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTAACCCCCAG

B

241 AAATCAACTBAAGCTGCTCCGCATCTCCCTGCTGATCCAGTCGTGGCTGAAGCCC leGinSerTrpLeuGluPro 100

GTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAAC

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22-MAR-1995
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21 LeuGlicGuGlySerAlaPheFroThr1eFroLeuSerArgLauPhoAepAanAlaSer_40			ment Scores: 5 No.: 10 nt Similarity: 93 Local Similarity: 93 Match: 92	by RFI. 2003-089799/1. From the Control growth and the Control of	12-WK-2000; 2000@a:0011459; 14-UK-2000; 2000@a:0011459; (UYMA-) UNIV MALES COLLEGE OF MEDICINE; COOPER DN. "Procter AM, Gregory J, Miller DS;	14-WAY-2001, 2001WO-GB002126.	-A2.	Key Location/Qualifiers Misc-difference 69 at 100 Misc-difference 69 at 100 Misc-difference 100 Misc Misc Misc Misc Misc Misc Misc Misc

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6 JU1719 standard: profeso: 217 AA	ACATTCT/GGCANCGTGAGTGCGCCCCTCTGGGAGGGCAGCTGTGGCTTC 606	GOCTAKTAHAANCTACGGCTGCTCTACTGCTTCAGGAAGGACKTGGACAAGGTGAAG GOCTAKTTAHAANCTACGGCTGCTCTACTGCTTCAGGAAGGACKTGGACAAGGTGAAG 	ACTGGGCAATCTTCAAGCAGACTWCAGCAGTTGGACGAAGCTGAGCAAGCATGAG ACTGGGCAATCTTCAAGCAGACTWCAGCAGTTGGACGAAAGCTGAGCAAGCATGAG TTTG1YG1N11ePheLymG1nThtTytSerLymPheAmpThtAmberH18AmhAppag 180	AGGARCTRANAGANAGGCATCANAGGCTSATWGGGAGGCTGGANGATTGGCAGGCCCCCGG 435	AGTRICTICACCAMAGACTAGATANACAGACCATCTTGACAGCAAGCAAGCATCTTGACCTCCTA 375	CTSCTCCCARCTTCCTSCTSCTCATCCATCATCATCATCCTSCAACCCCTTCCAGTTCCTCAGG 315	TOMARTINITYCGACACCTTCAACAGGAGGAAGGCAACGGAATGCAACTGCAACTYAGAG 255	- AACCCCCAGACCTCCCTTCGTTC 195 TyrileProLysGluGlnLysTyrLeuPheLeuGlnAsnProGlnThrSerLeuCysPhe 80	CTCCGCCCCATCGTCTGCACCAGCTGCCCTTTGACACCAGGAGTTT	

RESULT 6 AAU11719 AAU11719 d; procein; 217 AA.

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Growth hormone 1 gene (GH1), major isoform. 12-MAR-2002 (first entry)

AAU11719;

Growth homace i GHI, osteogathis, gene therapy; protein therapy; diabetes; obsets, vinteriton; coronagaly; observations received water recention; metabolic syndrome, mod disputs disorder; Growth hormone dynamiction; featibally prowth homace designation; short stature; pituitary storage defect; human; chromosome 17(3).

W0200185993-A2 Homo sapiens:

15-NOV-2001.

14-MAY-2001, 2001WO-GB002126

12-MAY-2000; 2000GB-00011459. 14-JUL-2000; 2000EP-00306004.

> Cooper DN, (UYWA-) UNIV WALES COLLEGE OF MEDICINE. Procter AM, Gregory J, Millar DS;

WPI; 2002-089798/12. N-PSDB; AAS18887.

Detecting growth hormone variants (GH1), useful in screening patients for growth hormone irregularities, comprises comparing the nucleotide

The dily variet described a subbed of describing varietien in growth homone continues to the continues of th US-09-856-796B-1 (1-609) x AAU11719 (1-217) Query Match: Best Local Similarity: Alignment Scores Percent Similarity Disclosure; Fig 6; 95pp; English sequence sequence of a GH1 gene sequence of the human (Sequence 217 AA 121 316 103 256 196 81 61 41 21 61 CTTCAAGAGGGCAGTGCCTTCCCCAACCATTCCCCTTATCCAGGCTTTTTGACAACGCTAGT MctAlaThrGlySerArgThrSerLeuLeuLeuAlapheGlyLeuLeuCysLeuProTrp TyrileProLysGluGlnLysTyrSerPheLeuGlnAsnProGlnThrSerLeuCysPhe CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT-----LeuGlnGluGlySerAlaPheProThrTleProLeuSerArgLeuPheAspAsnAlaSer ATGGCTACAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTCCCCCTGG AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA SerGluSerTleProThrProSerAsnArgGluGluThrGlnGlnLysSerAsnLeuGLu TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAAACAGAAAATCCAACCTAGAG LeuargalaHisargLeuHisGlnLeualaPheAspThrTyrGlnGluPheGluGluAla ServalPheAlaAsnSerLeuvalTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu LeuLeuArgIleSerLeu 93.09**1** 93.09**1** 92.58**1** 5.28e-89 1029.50 GHI from a test sample with that of a standard LeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg Gaps: Matches: Indels: Mismatches: Conservative: -----AACCCCCAGACCTCCCTCTGTTTC 255 60 40 100 80 140 375 120 315

376 ANGGACCTAGNGGANGGCATCCAAACGCTGATGGGGAGGCTGGANGATGGCAGCCCCCGG

me invention described a method of edecking variation in growth homome 1 (dH), and therefore off dysfunction in an individual: The method me the comprises comparing the manifested measures expense in coder to identify very tamp (dM) via wait, "The method is useful in accessing patients for growth homome irregularities of producing variant proteins for treating irregularities, and for the early described an opportunity would be irregularities, and for the early described an opportunity we would in management, of identified our detection method, particularly for described and appropriate variant patients of intellige defects and eurosphicibility to a disease such as dishered, chasticy or indection; for treating accessed by or signatum conditions effects on or indection; for treating accessed by or signatum conditions effects or indection; for treating accessed by or signatum conditions effects or indection; for treating accessed by or signatum conditions effects.

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Gregory J, Millar DS

2000GB-00011459: 2000EP-00306004. 2001WO-GB002126

N-PSDB; AAS18888 Cooper DN, 12-MAY-2000; 14-JUL-2000; 14-MAY-2001; 15-NOV-2001

growth hormone irregularities, com sequence of a GH1 gene from a test sequence of the human GH1.

nts (GH1), useful in screening patients comprises comparing the nucleotide test sample with that of a standard

Claim 20; Fig 7; 95pp; English. Detecting growth hormone variants WPI; 2002-089798/12 (UYWA-) UNIV WALES COLLEGE OF

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RESULT 7
AAU11720
ID AAU1
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                                                                                        /note= "Wild type Glu substituted by Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein, 217 AA
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AAU11730 standard; protein; 217 AA.

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determined, most and along disorders; disponding of dystingigins and cutation of the second of the s	ndromes, mood and sleep disorders; diagnosing GH dysfunction and	eful in gene therapy or protein therapy. The GH1 or GH variants are especially	used in the preparation of a medicament, diagnostics composition or	t, or detection kit. The method has the advantage of evanding the	ow spectrum of GH1 gene mutations; evaluating the role of GH1 gene	tations in the etiology of short stature; identifying of the mode of	nerilance of novel lesions; evaluation the effects of GHI mutations on	e structure and function of the GH molecule and days on the GH molecule	agnostic tests for inherital or desided and development of rapid	human growth hormone 1 (out) This sequence is a variant	numan growth hormone 1 (GH1), created from the GH1 wild type sequence	SCHEEN IN Figure 6 and one of many variations of the gene	scussed in the method of the invention	217	Scores:	5.28e-89 Length:	1029.50 Matches:	93.09# Congervative.	V: 93.09* Mismatcher	2: Darone Mismacches: (92.58% Indels:	Gaps:	· order	-796B-1 (1-609) - AMILIATO	-/96B-1 (1-609) x AAU11720		ATGCTACAGGCTCCCGGACGTCCCTGCTCCTCGCTTTTTTGCCTGCTCTCCTCCTCCT	- The contract of the contract	MetalaThrGlySerArgThrSerLeuLeuchalashen	 1 CTTCAAGAGGGGAGTGCCTTTCCGTTAGGTTTTCCGTTAGGTTTTCGTTTTTCGTTTTTCGTTTTTCGTTTTTCGTTTTTT	- CII CHAUNGSCHUITGCCTTCCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT	Leugh ng hag began a same a sa	accorning to the second and second the second secon	CTCCGCGCTCTTCTTCTACCTCCTCCTTTCTACTCTCTCT	TO THE CONTROL OF THE CANADA C	Legardy all sargless and all sargless are sargless and all sargless and all sargless and all sargless are sargless and all sargless and all sargless are sargless and all sargless and all sargless are sargless and all sargless are sargless and all sargless are sargless and all sargless are sargless and all sargless are sargless and all sargless are sargless and all sargless are sargless are sargless and all sargless are sargless and all sargless are sargless are sargless are sargless are sargless are sargless and all sargless are sargless are sargless are sargless are sargless are sargless are sargless are sargless are sargless are sargless are sargless are sargless are sargless are sargless are sargless are sargless are sargless are sargless are sargless are sa	5	1000000	- AACCCCAGACCTCCCTCTTTC	TVTT]=Pro[TyrileProLysGluGlnLysTyrSerPheLeuGlnAsnProGlnThrSerLeuCysPhe 8	TOTO COMPANY	TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAACCTAGAG		seroluserileProThrProSerAsnArgGluGluThrGlnGlnLysSerasnLenGln	CECCOCCOCCOCCOCCOCCOCCOCCOCCOCCOCCOCCOCC	CIGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCACC		LeuleuArgileSerLeuLeuLeuIleGlnSerTrpLeuGluProvalGlnPheLeuArg	ACTION OF THE PROPERTY OF THE	MGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA	SPTUS DE LE CONTROL DE LE CONT	GELVALFREM.LAMENSETLEUVALTYTG1yAlaSerAspSerAsnValTyrAspLeuLeu	ALCOHOLD COLOR COL	AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCCCC		wyswspreugiugiyileGinThrLeuMetGlyArgLeuGluAspGlySerProArg	ACTIVITO ON TOWN ON THE PARTY OF THE PARTY O	TO THE TOTAL CONTROL OF THE PROPERTY OF THE PR		ThrGlyGlnIlePheLysGlnThrTyrSerLysPheAspThrAsnSerHisbenZenZen 10	AT GENGAMISMATETAGEMENT AND AND AND AND AND AND AND AND AND AND	6 GCACTACTCAMGMACTACGGGCTGCTCTACTGCTTTCAGCAAGCACATTCCACTACGTTCCAC	55 STATE OF THE PROPERTY OF TH	Dalleuleul vegen Tyrol Villeur	ALGUEULEULYSASHTYrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu	TOTOTON AND AND AND AND AND AND AND AND AND AN	56	TO THE PROPERTY OF THE PROPERT			201 ThrPheLeuArglleValGlnCysArgSerValGluGlvSerCysGlvPho 217

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Comparisons, most and along discovers dissponing on definitions and custom in mag Prutters, stoogs, defens, The Gill veriants are specially contained in the preparation of a saturage, and sed of the state of the contained as a first kit, of detection kit. The method has the advantage of; copacing the contained as the first memorial contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the contained as the co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg
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                                                                                                                                                                                                                                                                                                                                                                      standard;
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93.09*
92.58*
                                                                                             eating disorder; polyimmunoglobulin receptor; pTgR
                                                                                                                                                                                                                                                                                                                                                                      protein; 217
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13-NOV-2000; 2000US-0248478P
14-NOV-2000; 2000US-0248819P
09-FEB-2001; 2001US-0267601P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complex useful for transporting series agent through epithelial harrier, has biologically active portion and target element directed to ligand that confers e.g. transporting properties to agent specific to ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABK81192.
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No.
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Matches: Conservative: Mismatches: Indels:

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CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT-----
                                                                                                                                                                                                                                                            CTTCANGAGGGCAGTGCCTTGCCAACCATTCCCTTATCCAGGCTTTTTGACAAGGCTAGT 120
                                                                                                                                                                                                                                                                                                                          MetAlaThrGlySerArgThrSerLeuLeuLeuAlaPheGlyLeuLeuCysLeuProTrp
                                                                                                                                                                                                                                                                                                                                                  CTGCTCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCGTGCAGTTCCTCAGG
                                                                                                                     TyrlleProLysGluGlnLysTyrSerPheLeuGlnAsnProGlnThrSerLeuCysPhe
                                                                                                                                                                                       LeuargalaHisargLeuHisGlnLeualaPheaspThrTyrGlnGluPheGluGluAla 60
                                                   SerGluser HeProThrPro
                                                                                      TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCGAACCTAGAG
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The invention described a method of descring variation is growth hormon careful, and hearefore all dysfunction in an individual, the method couldn't, and hearefore all dysfunction in an individual, the method care the care smaple with its than and section sequence of did gene obtained from the care smaple with its than and section and the control of the country. The method is gene expenses, in order to identify growth hormone irregularities or producing variant processes for trueing growth hormone irregularities or producing variant processes for trueing.	Claim 18; Page; 95pp; English.	Detecting growth homene watenie (GN1), useful in streening patients for growth homene frregularities, comprises comparing the deservation of a GRI gene from a test sample with that of a standard sequence of the Mannan GRI.	WPI; 2002-089798/12.	Cooper DN, Procter AM, Gregory J, Millar DS;	13-98X-2000; 200088-00011459. 141-2000; 20008E-0306004. 1798A-) UNIV WALES COLLEGE OF MEDITYING	14-MAY-2001; 2001WO-GB002126.	15-NOV-2001.	/notes "Wild type Val substituted by Ile" W0200185993-A2.	Key Location/Qualifiers Misc-difference 136	Synthetic.	Growth hormone dysfunction, familial growth hormone fales olsecter, short stature; pituitary storage defect; human; mutant; mutenh. Homo amiene	crowth hormone 1; GH1; osteopathic; gene therapy; protein therapy; diabetes; obesity; infection; acromegaly; gigantium, sodium retention; water retention; metabolic syndromes model signature.	Growth hormone 1 gene (GH1), V136I mutant.	12-MAR-2002 (first entry)	AAU11742;	AULI742 D AAULI742 standard; protein; 217 AA.	201 ThrPheLeuArg1leValGlnCy9Arg8erValGluGly8erCysGlyPhe 217	556 ACATTCCTGCGCATCGTGCAGTGCCGCTCTGGGGGGCAGCTGTGGGCTTC 606	181 Alabedeedyshanfyyddyshadleedfyrdysphaarriyshaadaadacanggroaag 555		ACTOGGCAGATCTTCAAGCAGACCTACACCAAGTTCGACACAAACTCACACAACGATGAC	141 LyahapteuglugluglyrilaginThrtauMetGilyArgiLauGilyaspilyGerProkrq 160	SerValPheAlaAenSerLeuValTyrGlyAlaSerAepSerAenValTyrAepLeuLeu	316 AGTETCTTCGCCAACAGCCTGGTSTACGGCGCCTCTGACAGCAACGTCTATAGCATCTCTA 175	101 Tautaniteritani
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OV -4.6 ACTRODECOMENTETRANSCHAFTCTSCHAFTCTSCHAFTCHAFTCHAFTCHAFTCHAFTCHAFTCHAFTCHAFT	Db 141 LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 160	121		256	OY .196 TCAGAGTCTNYTCCGACACCCTTCCAACAGGGGGGGAAGCCAACCGAAATTCCGACCTRCAG 255 Db . 81 SerGluserileProfurProferBarahryGluGluThrClrGlnLysSerFamLauGLu 100	Db 61 TyrTleProLyeGluGlnLyeTyrSerPheLauGlnAenProGlnThrSerLeuCyePhe 80		bb 41 LeukrydlaitakryteuijisGinlauka Bhaasmyk-rystaria kantonia 22	21 LeudinGluGlySerNlaPheProThrileProLeuSerArgLeuPheAepAsmAlaSer	9y 61 CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT 120	Oy 1 ANGCTHARACCTICCCGGARCTECCTGCTCCTTGGCTTTTGGCCTGCTCTCCCTGCGGGGGGG			93.09% Conservative:	No.: 6.58e-89 Length:	ì	cc discussed in the method of the invention. Note: This sequence does not CC appear in the specification but has been created from the GHI wild type CC sequence (AAU11719) given in figure 6		CC the etructure and function of the GH molecule and dovelopment of the mode of CC the etructure and function of the GH molecule and dovelopment of the GH molecule.					CC irregularities, and for the early detection and appropriate clinical (CC management of familial GH deficiency. The GHI variants are useful in	

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RESULT 11 AAU11726 compliance comparing the multiple of adjaceting variation in growth hormone (citil) and therefore of optimization in adjacet hormone comparing the multiple adjacet of the compliance comparing the multiple department of the large and control of the citil per detailed control of the citil per detailed control of the citil per detailed control of the citil per detailed control of the citil per detailed control of the citil per detailed control of the citil per detailed control of the citil per detailed control of the citil per detailed control of the citil per detailed period per detailed period of the citil per detailed period period of the citil period of the Growth hormone 1, GH1, outcopathic; gene therapy; protein therapy; diabetes to continue the accument of general section and disperses retention; the continue the accument of general seep disorder; steep disorder; steep disorder; steep thormone dysfunction; familial growth hormone deficiency; short stature; pictulary storage defect; human; mutant; mutenin. Growth AAU11726 standard; 12-MAR-2002 Detecting growth hormone variants (GHI), useful in screening patients growth hormone irregularities, comprises comparing the mucleotide sequence of a GHI gene from a test sample with that of a standard sequence of the human GHI. WPI; 2002-089798/12 Cooper 12-MAY-2000; 2000GB-00011459. 14-JUL-2000; 2000EP-00306004. 14-MAY-2001; 15-NOV-2001 WO200185993-A2 Misc-difference Synthetic Homo sapiens Claim 18; Page; 95pp; English (UYWA-) UNIV WALES COLLEGE OF MEDICINE 556 hormone 1 gene (GH1), I30V mutant ThreheLeuArgIlevalGinCysArgServalGluGlySerCysGlyPhe 217 ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC Procter AM, (first entry) 2001WO-GB002126 Location/Qualifiers /note= "Wild type Ile substituted by Val" protein; 217 Gregory J, Millar DS;

> Ş 8 ð 밝 S 밁 S 덩 S g

ğ 8888 Alignment Scores: Best Local Similarity: Percent Similarity: of human growth hormone 1 (GH1), one of many variations of the gene discussed in the method of the invention. Note: This sequence does not appear in the specification but has been created from the GH1 wild type sequence (AAULI719) given in figure 6 No.: Sequence 217 AA 6.58e-89 1028.50 93.09% 92.63% 92.49% Mismatches: Indels: Matches: Conservative:

Query Match:

US-09-856-796B-1 (1-609) x AAU11726 (1-217) 21 61 1 ATGGCTACAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTTGGCCTGCTCTGCCCTGG MetalaThrGlySerArgThrSerLeuLeuLeuAlaPheGlyLeuLeuCysLeuProTrp LeuGinGluGlySerAlaPheProThrValProLeuSerArgLeuPheAspAsnAlaSer 40 CTTCAAGAGGGGAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTTGACAAGGCTAGT 120 20

121 â CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT------------AACCCCCAGACCTCCCTCTTTC 195 17

8 S 121 ServaipheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 316 AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA тептетитат leserLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg

CTGCTCCGCATCTCCTGCTGCTCATCCAGTCGTGGCTGGAAGCCCGTGCAGTTCCTCAGG

436 141 376 ACTOGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAAACGATGAC AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg

495 160 435 140 375 120 315

201 181 496 161 ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC 606 GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAAGGACATGGACAAGGTCGAG ThrPheLeuArgTleValGlnCysArgSerValGluGlySerCysGlyPhe AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPhsArgLysAspMstAspLysValGLu ThrGlyGlnI lepheLysGlnThrTyrSerLysPheAspThrAsnSerHisAsnAspAsp 217

200 555 180

Š Db S ð

AAU11746 standard; protein;

217

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AAU11746

12-MAR-2002 (first entry

Growth hormone 1 gene (GH1), K194R mutant

22282925 508282925 Growth hormone 1; GH1; osteopathic; gene therapy; protein therapy; diabetes; obesity; infection; acromegaly; gigantism; sodium retention;

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Alignment Pred. No.: Score: Score: Percent Si Best Local Query Matc DB;	SO	Š																ននន	8 \$ 8	2223	725	Z S	e X	2 2	- - - - - - - - - - - - - - - - - - -	ž P	S Z	X P	FFS	ΞX	88	X Z Z	Š
Scores: 1.02e-88 1026.50 milarity: 93.094 Similarity: 92.634 h: 52.314	Sequence 217 AA;	The state of the s	appear in the specification but has been created from the GHI wild type	discussed in the method of the inves	diagnostic tests for inherited GH d	inheritance of novel lesions; evalu	mutations in the etiology of short	kit, or detection kit. The method h	be used in the preparation of a med	determining pituitary storage defec	syndromes, mood and sleep disorders	with lactogenic, diabetogenic, lipo	binding defects and susceptibility	management of familial GH deficience therapeutic, diagnostic or detection	irregularities, and for the early d	variation (GH1 variant). The method growth hormone irregularities or no	test sample with a standard human (1 (GH1), and therefore GH dysfunction in an individual.	Claim 18, Page, 95pp, English.	growth hormone irregularities, comprises comparing the sequence of a GH1 gene from a test sample with that of sequence of the human GH1.	Detection		DN Proctor and	(UYWA-) UNIV WALES COLLEGE OF MENT	12-MAY-2000; 2000GB-00011459. 14-JUL-2000; 2000EP-00306004.	14-MAY-2001; 2001WO-GB002126.	15-NOV-2001.	WO200185993-A2.	c-difference		Homo sapiens. Synthetic.	Growth hormone dysfunction; familial short stature; pituitary storage def	Water retention, metabolic
Length: 217 Westches 201 Commonwhive: 201 Wismarches: 0 Indels: 0			been created from the GH1 wild type	of many variations of the gene	eficiency. This semience is a variant	ation the effects of GH1 mutations on	evaluating the role of GH1 gene	as the advantage of: expanding the	be used in the preparation of a medicamont discussion of Wariant may also	ts. The GH1 variants are especially	conditions associated with sodium and water retention, metabolic syndromes, mood and sleep disorders.	ly or gigantism conditions associated	to a disease such as disbetes, obesity	y. The GHI variants are useful in	etection and appropriate clinical	is useful in screening patients for	standard human GH1 gene sequence in order to the	Anvention described a method of detecting variation in growth hormone 3H1), and therefore GH dysfunction in an individual. The method		(GH1), useful in screening patients for prises comparing the nucleotide sample with that of a standard		, Millar DS;	CINE				,		Another "Wild type Lye substituted by Arg"	4	1	mood dis growth h ect; huma	Fav.

US-09-856-796B-1 (1-609) x AAU11746 (1-217)

Gaps:

14-MAY-2001; 2001WO-GB002126 15-NOV-2001

W0200185993-A2

Misc-difference 194

/note= "Wild type Lys substituted by Glu"

Synthetic.

cmo sapiens.

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RESULT 13
AAU11747
Growth homems 1; GHI; osteopathic; gene therapy; protein therapy; diabetes; obsetly; infertion; carcengaly dispartisms sodium retention; water retention; metabolic printense and dispartisms of disorder; along disorder; of crowth homemo deprintention; fainting speech homemo desiredemory; short stature; pituitary storage defect; human; mutan; mutan; mutan;
                                                                                                                                      Growth hormone 1 gene (GH1), K194E mutant.
                                                                                                                                                                                               12-MAR-2002
                                                                                                                                                                                                                                                                    AAU11747 standard; protein; 217 AA.
                                                                                                                                                                                                                                          AAU11747
                                                                                                                                                                                                                                                                                                                                              556 ACATTCCTGCGCATCGTGCAGTGCGGCTCTGTGGAGGGCAGCTGTGGGTTC 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 -----AACCCCCAGACCTCCCTCTGTTTC 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TyrIleProLysGluGlnLysTyrSerPheLeuGlnAsnProGinThrserLeuCysphe 80
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The underly admitted a method of detecting writistion is growth hormone controlled to the controlled t 88888888888 US-09-856-796B-1 (1-609) x AAU11747 (1-217) Query Match: Percent Similarity: Best Local Similarity: Pred. No. 12-MAY-2000; 2000GB-00011459-14-JUL-2000; 2000EP-00306004. Detacting growth hormone variants (GHI), useful in acreening patients growth hormone irregularities, comprises comparing the nucleotide sequence of a GHI game from a test sample with that of a standard sequence of the human GHI. (UYWA-) UNIV WALES COLLEGE OF MEDICINE Claim 18; Page; 95pp; English Sequence 217 AA; 61 TyriierchysGluGlnLysTyrSerPheLeuGlnAsnProdinThrSerLeuCysPhe 172 121 ÷ 21 61 CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT------171 CTTCAAGAGGGCAGTGCCTTCCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT 120 MetAlaThrGlySerArgThrSerLeuLeuLeuAlaPheGlyLeuLeuCysLeuProTrp ATGGCTACAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTTGGCCTGCTCTGCCTGG 60 LeuargalahisargieuhisGinLeualapheAspThrTyrGinGiupheGluGluAla 60 LeuGinGluGlyScralabheProThrIleProLeuSerargLeuPheAspAsnAlaSer Procter AM, 1.27e-88 1025.50 93.09% 92.63% 92.22% Gregory J, Millar DS; Mismatches: Gaps: Indels: Conservative: Matches -- AACCCCCAGACCTCCCTCTGTTTC 195 20 ô 80

196

TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAACCTAGAG 255

The invention described a method of detecting variation in growth hormone

RESULT 14 AAU11735 δ 밁 ફ 胺 Q 벙 밁 g S 당 ž ž Growth hormone 1, GHI; estempathic, gene thermy; proceint thermy; diabetes; obsity; infection; accommonly; gipenties; sodium returnion; water returnion; seaboblic synthal growth hormone deficiency; drowth hormone dystimction; deathilal growth hormone deficiency; short estempes; accept defect; human; mutant; mutain. AAU11735 standard; protein; 217 AA Misc-difference 100 Synthetic Growth hormone 1 gene (GH1), E100K mutant 12-MAR-2002 Detecting growth hormone variants (GH1), useful in screening patients growth hormone irregularities, comprises comparing the nucleotide sequence of a GH1 gene from a test sample with that of a standard sequence of the human GH1. Cooper DN, (UYWA-) UNIV WALES COLLEGE OF MEDICINE 12-MAY-2000; 2000GB-00011459 14-JUL-2000; 2000EP-00306004 14-MAY-2001, 2001WO-GB002126 15-NOV-2001 WO200185993-A Homo sapiens Claim 18; Page; 95pp; English WPI; 2002-089798/12. 141 LysaspieuGluGluGlyTleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 160 256 CTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG 315 201 556 ACAPTROCTGCGCATCGTGCAGTGCCACTCTGTGGAGGGCAGCTGTGGCTTC 606 181 161 436 ACTOGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACAACTCACAACGATGAC 495 el SerGluSerIleProffirProSerAenArgGluGluThrGlnGlnLyeSerAenLeuGlu 100 AAGGACCTAGAGGAAGGCATCCAMACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG 435 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgGluAspMetAspLysValGlu Procter AM, (first entry) /note= "Wild type Glu substituted.by Lys" Location/Qualifiers Gregory J, Millar DS; 180

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181 AlaLeuLeuLyrAenTyrGlyLeuLeuTyrCyrPheArgLyrAepWetAepLyrWalOlu 200
                     161 ThrGlyGlnIlePheLysGlnThrTyrSerLysPheAspThrAsnSerHisAsnAspAsp 180
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201 556 ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC ThrPheLeuArgIleValGinCysArgSerValGluGlySerCysGlyPhe 217

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AAU11744 RESULT 15 AMU11744 standard, protein, 217 AA

AAU11744;

12-MAR-2002 (first entry)

Growth hormone 1 gene (GH1), Al81V mutant.

2 ğ diabetes, obesity, infection, earnegaly, gigantism, sodium retention, water retention, metabolic syndrose mood disorder; step disorder, fororth hormone dysfunction, familial growth hormone dysfunction, familial growth hormone dysfunction, familial growth hormone dysfunction, familial Growth hormone 1; GH1; osteopathic; gene therapy; protein therapy; pituitary storage defect; human; mutant; mutein

Synthetic Homo sapiens.

Misc-difference 181 Location/Qualifiers

/note= "Wild type Ala substituted by Val

W0200185993-A2

12-MAY-2000; 2000GB-00011459 14-MAY-2001; 2001WO-GB002126

(UYWA-) 14-JUL-2000; 2000EP-00306004. UNIV WALES COLLEGE OF MEDICINE

Cooper , אַמ Procter AM, Gregory J, Millar DS;

WPI; 2002-089798/12

Detecting growth hormone variants (GHI), useful in screening patients for growth hormone irregularities, comprises comparing the nucleotide sequence of a GHI gene from a test sample with that of a standard sequence of the human GHI.

Claim 18; Page; 95pp; English.

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¥8888888888888888888 in the invention described a method of detecting variation is grown become control (GHI), and therefore off optionation in an individual, inspection of the case maybe control to maintenance agents of cent is one to describe the maintenance of the gene detained from the control of the contro

¥888888888 where processing of only some marketons, evaluating the note of offill game intertained in the schology of short scenario distributed the schology of short scenario distributed the schology of short schology of short schology of short schology of short schology of the s

Sequence 217 AA;

Mismatches: Conservative: Indels:

US-09-856-796B-1 (1-609) x AAU11744 (1-217)

556 181 161

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Search completed: Pebruary 6, 2005, 13:21:32 Job time: 133.5 secs

121 256 196 TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGGAAATCCAACCTXGAG 496 GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGACATGGACAAGGTCGAG 555 436 ACTGGGCAGATCTTCAAGCAGCCTACAGCAAGTTCGACAAACTCAGACAACGATGAC 495 141 376 АЛССАССТАСЛОВАНОСТАТССЬВАСССТСВАТССОСАСССТССВАССТСССВО 435 81 61 TyrileProLysGluGlnLysTyrSerPheLeuGlnAsnFrodinThrSerLeuCysPhe 80 41 LeukrgkiahishrgLeuHisGinLeukiaPhekspThrTyrGinGluPheGluGluAla 60 21 61 LeuleuhrgileSerLeuLeuLeulleGinSerTrpLeuGluproVelGinPheLeuhrg 120 LeudindiudiyseralabhebroThrTleBroLeuSerArgLeuBheAepAsnAlaSer 40 CITCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTTGACAACGCTAGT 120 LysaspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 160 crecrececarcrecrecrecrecrecrecarccaerceregeregaecccerecaericcreaes 315 SerGluSerIleProThrProSerAsnArgGluGluThrGlnGlnLyeSerAsnLeuGlu 100 ACATICCIGCGCAICGIGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC 606 ValLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu ThidlyGlnIlePheLyeGlnThrTyrSerLysPheAspThrAsnSerHisAsnAspAsp 1.27e-88 1025.50 92.63* 92.63* 92.22*

255

Percent Similarity: Best Local Similarity: Query Match: so Alignment Scores: Pred. No.:

1 1023-5 92.6 217 1 US 01-469-513 2 Sequence 51. Appl 1 1023-5 92.6 217 2 US 01-469-515-1 2 Sequence 51. Appl 2 1023-5 92.6 217 2 US 01-469-515-1 2 Sequence 51. Appl 1 1023-5 92.1 217 3 US 01-590-201-1 0 Sequence 10 Appl 1 1023-5 92.1 217 3 US 01-590-201-1 0 Sequence 10 Appl 1 1023-5 92.1 217 3 US 01-790-201-1 0 Sequence 10 Appl 1 1023-5 92.1 217 3 US 01-790-201-1 0 Sequence 10 Appl 1 1023-5 92.1 217 3 US 01-790-201-1 0 Sequence 1 Appl 1 1023-5 92.1 217 3 US 01-790-201-1 0 Sequence 1 Appl 1 1023-5 92.1 217 3 US 01-790-201-1 0 Sequence 2 Appl 1 1023-5 92.1 217 3 US 01-790-201-1 0 Sequence 3 Appl 1 1023-5 92.1 217 3 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 218 3 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 218 3 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 218 3 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 218 3 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 218 3 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 218 3 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 218 3 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 218 3 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 218 3 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 2 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 2 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 2 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 2 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 2 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 2 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 2 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 2 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 2 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 2 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 2 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 2 US 01-790-201-1 0 Sequence 5 Appl 1 1023-5 92.1 2 US 01-790-201-1 0 Sequence 6 Appl 1 1023-5 92.1 2 US 01-790-201-1 0 Sequence 6 Appl 1 1023-5 92.1 2 US 01-790-201-1 0 Sequence 6 Appl 1 1023-5 92.1 2 US 01-790-201-1 0 Sequence 6 Appl 1 1023-5 92.1 2 US 01-790-201-1 0 Sequence 6 Appl 1 1023-5 92.1 2 US 01-790-201-1 0 Sequence 6 Appl 1 10	9.0	Dischase Issued Patents AA.	ODGLE-frame, "Dig nobel": OMYALD ON COMMAND, DEROS (1987) ON COMMAND	Post-processing Miximum Match 10% Listing Miximum Match 10% Listing first 45 summaries	Total number of hits satisfying chosen parameters: 1027090 Middimum DB seq length: 0000000000	74649064	o o in in	Patfact acore: 112 Sequence: 1 atggctacaggetccoggacagggcagctgtggcttctag 609	xum on: February 6, 2005, 13:14:50; Search time 31 Seconds (Without alignments) 293:88 Willion cell updates/sec	eic - protein search, using frame_plu	Copyright (c) 1399 - 2005 Compagen Ltd.
SOFTWARE: 41:55	ible S/MS-DOS	APPLICANT: LOUGHERD, ARMS UTRICAN APPLICANT, Exace, The Las APPLICANT, Exace, The Las TITLE OF ENTENTION. Depoyed method for the TITLE OF ENTENTION. Decision WIMMERS OF SECURITIES; 50 ADDRESSEE: Fish & Elcharden STREET, 235 Franklin Streen	72.0 198 4 72.0 198 4 9281 9281 94710N:		884.5 79.5 401 4 881.5 79.3 191 4 880.5 79.2 177 1 880.5 79.2 177 2	888.5 79.9 197 4 888.5 79.9 197 4	80.2 241 3 80.2 241 3 80.2 245 4 80.2 448 4 79.9 197 4	891.5 80.2 191 4 891.5 80.2 192 1 891.5 80.2 194 2	81.7 176 3 81.7 176 3 80.6 191 3	16 924.5 83.1 360 3 US-08-784-582- 16 924.5 83.1 274 3 US-08-794-582- 17 914 82.2 176 3 US-08-77-728- 18 914 82.2 176 3 US-08-990-774-	89.8 198 2 89.8 198 4

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Pred. No.:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 217 animo
                                                                                US-08-469-658-51
                                             Sequence 51, Application US/08469658
Patent No. 5917018
GENERAL INFORMATION: ,
APPLICANT: Th eger
APPLICANT: Holtet,
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Mismatches:
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US-08-469-658-51
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SEQUENCE CHARACTERISTICS:
LENGTH: 217 amino acid
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Fish & H
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NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKST NUMBER: 06
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CURRENT APPLICATION DATA:
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TELEPHONE: 617 542 5070
TELEPAX: 617 542 8906
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FILING DATE: June 5, 1995
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CLASSIFICATION: 530
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93.09*
92.58*
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06363/002002

Conservative: Mismatches: Indels: Matches: Gaps

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----AACCCCCAGACCTCCCTCTGTTTC 195

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APPLICANT: Etzerod, IMPROVED TITLE OF INVENTION: PROTEINS TITLE OF GEOGIENCES: 58
E: Fish & Richardson P.C.
225 Franklin Street
                                                                                              IMPROVED METHOD FOR THE REPOLDING OF
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Alignment Scoree: 1.19e-95 Longth: 217 Score: 1024:50 Matches: 201 Percent Similarity: 92.834 Conservative: 0	INFORMATION FOR SEG IN NO. 10. SECURING LANGUAGESSATICS TO TREBUTE 227 mains acide STRANDINGSES NO. 4 STRAND	ATTORNEY/AGENT INFORMATION: NUME: HIGHAIN ACT. SEC. AT TO. ACT. ACT. ACT. ACT. ACT. ACT. ACT. ACT	APPLICATION WOMER: US/08/589,028 FILING DATE: Concurrently Herewith CLASSFICKTION: 435	COMPUTER: 1BM PC Compatible OPERATING SYSTEM: PC-DOS/Ms-DOS SOFTMARE: PatentIn Relades #1.0, Version #1.30	J COMPTRY: USA ZIE: 77210-433 COMPUTER READABLE DORY: MEDIUM TYPE: Ploopy disk	J ADDRESSEE Arnold, White & Durkee 5 STREF: P. O. Box 4433 1 CITY: HOUSEON 5 STREE: TX	TITLE OF INVENTION: Recombinant Expression of Proteins From TITLE OF INVENTION: Seretory Cell Lines NUMBER OF SEQUENCES: 50 CORRESPONDENCE AUGUSTS: 50 CORRESPONDENCE AUGUSTS:	APPLICANT: Clark, Samuel A. APPLICANT: Mispen, Anice S. APPLICANT: Quade, Christian APPLICANT: Quade, Christian APPLICANT: Knue, Pred	JOHNBAL INFORMATION: APPLICANT: Newgard, Christophor B. APPLICANT: Halban, Philippe APPLICANT: Halban, Philippe APPLICANT: Halban, Philippe APPLICANT: No. 6071228mington, Karl D.	resULT 3 3 US-08-599-028-10 US-08-599-028-10 US-08-599-028-10 Application US/08589028 Fatent No. 6087129	b 201 ThrPhoLeuArg1leValGinCyaArgserValGiuGlySerCysGlyPha 217	181	161	bb 141 JORGEN AUGUST CONTROL OF THE TOTAL OF	121 ServalbhealadanSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu	Db 101 IndicentegliesGertentententledinstripplandstrippsgegenetentententging
AUDMESSES: Arnold white & Durkee FYREN: P.O. Box 4433 CTY: Houseon Ox 443 SYME: Texas COUNTRY: UgA ACRE TYTAIN	APPLICANT: OLIMPOT, MILES S. APPLICANT: MCMESTER, TEAMS PROFILE IN APPLICANT: MCMITTY, DOMING THE APPLICANT: MCMITTY, DOMING THE APPLICANT: MCMITTY, DOMING THE EXPRESSION OF PROTEINS FROM INTIME OF SECURENCES INCLUDENCES		RESULT 4 US-08-784-582-10 is Sequence 10 and ication to footness	Oy 556 ACATTCTTCCOATCOTTCAGCTCTTCTCAGGGCAGCTGTGGCTTTC 606	Oy 495 GOACTACTOMAGACTACOGCTCCTCACTCCTTCCAGGAAGGACATGGACAAGGTCGAG 555	Oy 415 ATTOGCOGATTTOWACCIGACTTCACCACCACCACCACCACCACCACCACCACCACCAC	Oy 376 AAGANCTARAGAAGCCNTCSAAGCTTGSTGGGGAAGCTTGGAAGATGGCAAGCTCCCCGG 435	Oy 3.6 AGTSTCTTCGCAACAGCTCTSTSACGGGGCCTCTABAGCAACGTCTATGACCTCTA 375 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	101	Oy 196 TOMANTYATACANACCTICAMANDACAMANTACHACHTANAC 255	OY 172	Or 121 CTCCGCGCCCATONYCTGCACCAGCTGCCCTTGCACCCTGCCGAGGGTTT		1 A NOBETHALAGET COCCOALOGY COTTON CONSECUTIVE CONCENTRACE COCCOSC 6 1	-09-856-7	Best Jocal Similarity: 92.53t Minaschws: 1 Onory Match: 92.13t Indias: 15 DB: 3

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US-09-856-796B-1 (1-609) x US-08-784-582-10 (1-217)
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Best Local Similarity:
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SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 0:
PILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:514
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436 ACTGGGGAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC 495
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                                                                                                                                                                                                                                    ServalPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 140
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                                                                                                                                                     ANGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG 435
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512/474-7577
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Indels:
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US-08-785-271-10
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                                         US-09-856-796B-1 (1-609) x US-08-785-271-10 (1-217)
                                                                                         Query Match:
                                                                                                                                                                      Alignment Scores:
                                                                                                         Best Local Similarity:
                                                                                                                         Percent Similarity:
                                                                                                                                          Score:
                                                                                                                                                          Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/785,271
APPLICATION NUMBER: US/08/785,271
FILING DATE: CONGULTERLLY HETEWICH
CLASSIFICATION: 047
ENIOR DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
TITLE OF INVENTION: SECRETORY CELL LINES
                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/589,028
FILING DATE: 19-UAN-1996
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 217 amino acid
                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Houston
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                                                                                                                                                                                                                                                                                                                                                                             NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                       TYPE: amino acid
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USA
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Quaade, Christian
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                                                                                             1.19e-95
1024.50
92.63*
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92.13*
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                                                                                                                                                                                                                                                                                                                                                                       UTSD: 513
                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                             Matches:
                                                                                   Gaps:
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guProTrp 20

CTTCAAGAGGGAGTGCCTTCCCAACCÁTTĆCCTTATCCACGCTTTTTGACAACGCTAGT

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THE PERSON NAMED IN

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RESULT 6
US-08-759-628-11
; Sequence 11, App
; Patent No. 6225
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Patent No. 6225446
GENERAL INFORMATION:
                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                          ZIP: W940K-1104
COMPUTER READMARE POMH;
MROINN TIPE: FLORPY disk
MROINN TIPE: FLORPY disk
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READMARE SOZIEN: FLORPY-DIS
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SOZIEN: FLORPY-DISK
MROINN TAPLICATION NAMERS: US/80/759.G28
FFILING DATE: 05-80C-1998
FFILING DATE: 05-80C-1998
COMPANDED
TO THE TOPLICATION NAMERS: US/80/759.G28
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAK Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
SIATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT, Alteann, Scott W.
APPLICANT, Alteann, Stephando,
APPLICANT, Beath, J. Fernando,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ТСАGAGTСТАТТСССАНСАСССТССАЛСАGGGAGGAAACACAACAGAAATCCTAGCCTAGAG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TyrIleProLysGluGlnLysTyrSerPheLeuGlnAsnProGlnThrSerLeuCysphe
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                                                                           US 60/008,574
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161 436 141 376 316

ThrolyGinIlePhetysGinThrTyrSerLysPheAspThrAsnSerHisAsnAspAsp ACTGGGGAGATOTTCAAGCAGACCTACAGCAAGTTGGACACAAACTCACACACGATGAC AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCGG SerValPheAlaAenSerLeuValTyrGlyAlaSerAepSerAenValTyrAepLeuLeu AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA

uGlyIleGlnThrLeuMetGlyArgLeuG

LuAspGlySerProArg

495 160 435 140 379 120 315 100 25 80

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81 61 4

196 172

101 LeuLeuArgiieSerLeuLeuLeuileGinSerTrpLeuGiuProValGinPheLeuArg 256 GTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGAGCCCGTGCAGTTCGTCAGG

SerGluser HerrothreroserAsnArgGluGluThrGlnGlnLysSerAsnLeuGlu TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAGAAATCCAACCTAGAG TyrileProLysGluGlnLysTyrSerPheLeuGlnAsnProGlnThrSerLeuCysPhe Ę 8

> 21 LeuGinGiuGlySeralapheProThrIleProLeuSerArgLeuPheAspAsnAlaMet 61 CTTCARGAGGGCATGCCTTCCCCAACCATTCCCTTATGCAGGCTTTTTTGACAACGCTAGT 120

MetAlaThrGlySerArgThrSerLeuLeuLeuAlaPheGlyLeuLeuCyaLeuProTrp ATROCTACAGOCTCCCGGACGTCCCTCCTCGCTTTTGGCCTCCTCGCTCTCCTCGC

CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT------- AACCCCAGACCTCCCTCTTTTC 19

17 40 20 60

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US-09-856-796B-1 (1-609) x US-08-759-628-11 (1-217)
                                         Query Match:
                                                  Percent Similarity:
Best Local Similarity:
                                                                                    Pred. No.:
                                                                                             Alignment Scores:
                                                                                                                    US-08-759-628-11
                                                                           Score:
                                                                                                                                                                                                                                                                                                                                                    TELEPAX: 415-852-9196
TELEPAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                             LOCATION:
FEATURE:
                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                  FEATURE:
NAME/KEY;
                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                               OTHER INFORMATION:
                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                      LOCATION:
                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                  LENGTH: 217 amino acids
                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: DX0552Q
                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                  Peptide
192..210
                                                                                                                                                                                    Peptide
133..153
                                                                                                                                                                                                                    Peptide
94..115
                                                                                                                                                                                                                                                    Peptide
32..53
                                                                                                                                                                                                                                                                                                  linear
                                    1.19e-95
1024.50
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                                                                                                                         /note= "The peptides ;
depicted in Figure 1"
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                                  Conservative:
Mismatches:
Indels:
                                                                  Length:
Matches:
                         Gaps:
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436 ACTGGGCAGATCTTCAAGCAGAGCTACAGCAAACTCGACACAAACTCACACAAACGATGAC 495

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1
LENGTH: 217
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09284878
Patent No. 6342375
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NewICOMT: Saldama, Bugo Barrona
HITIB OF PROPRIED Jose Maria Videlind websjotrophic P. pastoria Yeant
HITIB OF PROPRIEDS: Semantician and Secretion of the Buman Growth Hormone
Fill Refresents: 1899-00100100
CHESSEN PROPRIEDS: 1009/07/08/07/0010
CHESSEN PROFILORION WEBSEN 199/29/00103
FRIEDS PROFILORION WEBSEN 199/29/00103
FRIEDS PROFILORION WEBSEN 199/29/00103
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                                                                                    <121 ServalphehlansnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu</p>
141 Lynhapteudiudludlylledlminiteuweudlyhrgiaudlunapdly8erProArg 180
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92.63%
92.63%
92.13%
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Indels:
Gaps:
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SerGluSerTleBroThrProSerAsnArgGluGluThrGlnGlnLysSerAsnLeuGlu 100 TCAGNGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAACCTAGAG 255 TyrIleProLysGluGlnLysTyrSerPheLeuGlnAsnProGlnThrSerLeuCysPhe LeuargalaHisargLeuHisGinLeualaPheAspThrTyrGinGluPheGluGluAla 60

CTGCTCCGCATCTCCCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG 315

leSerLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg 120

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316 AGYGYGTYTGGCGAACAGCTGGTGTACAGGCGCTCTGACAGGAACGTCTATGACCTCCTA 375

LeuLeuArgI

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CHEST REFERENCE, FRANCE 105/09/939,918
CHEST REPLACATION NAMESE: US/09/939,918
CHEST FILLING DATE: 2001-08-15
PRICE APPLICATION NAMESE: 99/918-18
PRICE FILLING DATE: 1989-05-25
NAMESE OF SED 10 NOS: 11 Indoor Version 4.0
SOPTHAME: FastSQL for Windows Version 4.0
SOPTHAME: FastSQL for Windows Version 4.0
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                                                                                                                                                                        US-09-856-796B-1 (1-609) x US-09-929-918-9 (1-217)
                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                            US-09-929-918-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent NV. GENERAL INFORMATION: GENERAL INFORMATION: Kordyum, Vitaliy A. APPLICANT: Chertykh, Svitlana I. APPLICANT: Chertykh, Jryna Yu. Slavchenko, Iryna Yu.
                                                                                                                                                                                                                                                  Best Local Similarity:
                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Slavchenko, Iryna Yu.
APPLICANT: Vozianov, Oleksandr
ITILS OF INVENTION: FRAG-ERROBENT SUBER PRODUCTION OF
ITILS OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEFTIDES
                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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Matches:
Conservative:
Mismatches:
Indels:
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ANGGNCCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG 435 SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 140 LysaspheuGluGluGlyileGlnThrLeuMetGlyargheuGluaspGlySerProarg 160

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US-09-856-796B-1 (1-609) x US-08-187-756C-4 (1-217)
                                                                                                Percent Similarity:
-Best Local Similarity:
Query Match:
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Pred. No.:
                                                                                                                                              Score:
                                                                                                                                                                                                      JS-08-187-756C-4
                                                                                                                                                                                                                                                                                    TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                     PELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/187,756C
FILING DATE: January 27, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS-DOS
      AMINO ACID
                                                                                                                                                                                                                                  LINEAR
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Conservative:
Mismatches:
Indels:
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Patent No. 5962411
                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Rosen,
                           APPLICATION NUMBER: US 08/187,756
FILING DATE: 27-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                       PRIOR APPLICATION DATA:
                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
AURIST APPLICATION DATA:
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
REGISTRATION NUMBER:
                                                                                      APPLICATION NUMBER: US/08/710,324A
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
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CITY: Rockville
                                                                                                                                                                                                                               ZIP:
                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Sciences, Inc
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161 436 ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC 495 141 376 AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG 121 ServalPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 316 AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA 101 256 CTGCTCCGCATCTCCCTGCTGCTCATCCAGTGGTGGCTGGAAGCCCGTGCAGTTCCTCAGG 315 196 TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAACAGAATCCAACCTAGAG 255 172 81 61 ThrGlyGlnIlePheLysGlnThrTyrSerLysPheAspThrAsnSerHisAsnAspAsp LysAspLeuGluGluGlyIleGinThrLeuMetGlyArgLeuGluAspGlySerProArg LeukeukrgIleSerLeukeuEeuIleGlnSerTrpLeuGluProValGlnPheLeukrg 120 SerGluserTieProThrProSerAsnArgGluGluThrGlnGlnLysSerAsnLeuGlu 100 TyrIleProLysGluGlnLysTyrSerPheLeuGlnAsnProGinThrSerLeuCysPhe 80 -AACCCCAAACCTCCCTCTTTTC 19s LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPheGluGluAla 60

180 160 435 140 375 RESULT 9 US-08-187-756C-4

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121 CTCCGGGGCCCATCGTCTGCCACCAGCTGGCCTTTGACACCTACCAGGAGTTT-----171

CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT 120 LeuGlnGluGlySerAlaPheProThrIseProLeuSerArgLeuPheAspasnalaSer

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ThreheLeuargileValGlnCysargSerValGluGlySerCysGlyPhe 217

Sequence 4, Application US/08187756C Patent No. 5597709

GENERAL INFORMATION:

TITLE OF INVENTION: Human Growth Hormone NUMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD

COUNTRY: CITY: ROSELAND

ASD

07068 NEW JERSEY

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Best Local Similarity:
Query Match:
DB:
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INFORMATION FOR SED ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 217 AMINO ACIDS
TYPES: MAINO ACID
STRANDEDNESS:
RESULT 11
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TELEPHONE: 301-309-8504
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MOLECULE TYPE: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
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                                                                                                      AlaLeuLeuLysAsnTyrGlyLeuLsuTyrCysPheArgLysAspMetAspLysValGlu
                                                                                                                                    ThrGlyGlnIlePheLysGlnThrTyrSerLysPheAspThrAsnSerHisAsnAspAsp
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1016.50
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Mismatches:
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 217 AMINO ACIDS

TELECOMMUNICATION INFORMATION: TELEPHONE: 301-309-8504 ATTORNEY/AGENT INFORMATION: PRIOR APPLICATION DATA:
APPLICATION NUMBER:

301-309-8439

NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: PF104D1.SKB

TOPOLOGY: LINEAR MOLECULE TYPE: PRO

PROTEIN

STRANDEDNESS

AMINO ACID

8 0 ...

7.74e-95 1016.50 92.17% 92.17% 91.41%

Mismatches: Indels: Conservative: Matches: Length: MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-COOS/MS-DOS
OPERATING SYSTEM: PC-COOS/MS-DOS
SOFTMARE: PATENTIAN REPERATED SYSTEM
APPLICATION NUMBER: US/09/411,657

Version #1.30

CLASSIFICATION:

FILING DATE: FILING DATE:

08/710,324

COMPUTER READABLE FORM:

ZIP: 20850 COUNTRY: CITY: Rockville

ě

USA

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: 1
ADDRESSES: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue TITLE OF INVENTION: Human Growth Factor

US-09-411-657-4 v

256 196 172

CTGCTCCGCATCTCCCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG 315 SergiuserileProThrProSerAsnArgGluGluThrGlnGlnLysSerAsnLeuGlu 100

nserTrpLeuGluProValGinPheLeuArg 120

316 AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGGAACGTCTATGACCTCCTA 375

ANGGCTACAGGCTCCCGGACGTCCCTGCTCTGGCCTTTTTGGCCTGCTCTGCCCTGG 60

41

61 TyrileProLysGluGlnLysTyrSerPheLeuGlnAsnProGlnThrSerLeuCysPhe

80

TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAACCTAGAG 255 -AACCCCCAGACCTCCCTCTGTTTC 195 LeuargalaHisargLeuHisGinLeualaPheaspThrTyrGinGluPheGluGluAla 60

Sequence 4, Application US/09411657 Patent No. 6566328, GENERAL INFORMATION: APPLICANT: "Rosen, et al.

SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu

20

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US-09-856-796B-1 (1-609) x US-08-187-756C-5 (1-198)
                                                                                                       query Match:
                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                           Score:
                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                         US-08-187-756C-5
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US-08-187-756C-5
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                                                                                                                                                                                                                                                                                   TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 AMINO ACIDS
TYPE: AMINO ACID
STRENDERSEC
                                                                                                                                                                     . No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/187,756C
FILING DATE: January 27, 1994
CLASSIETCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, I
ADDRESSEE: CECCHI, ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ROSEN, ET AL.
TITLE OF INVENTION: Huma
                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                     NAME: PERBARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
   201 ThrPheLeuArgileValGlnCysArgSerValGluGlySerCysGlyPhe 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            556 ACATTCCTGCGCATCGTGCAGTGCGGCTCTGTGGAGGGCAGCTGTGGCTTC 606
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SE: CECCHI, STEWART & OLSTEIN
6 BECKER FARM ROAD
                                                                                                                                                                                                                                                        LINEAR
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999.00
97.03#
97.03#
89.84#
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                                                                                             Matches:
Conservative:
Mismatches:
Indels:
                                                                               Gaps:
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                                                                                                                            COMPUTER READMAGE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ITM PC compacting
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMANE: Pacentin Release $1.0, Ver
RETURN APPLICATION DATA:
APPLICATION MOMBER: US/86/710,324A
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08710324A
Patent No. 5962411
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/187,756
FILING DATE: 27-JAN-1994
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosen, et al.
TITLE OF INVENTION: Human Growth Factor
                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
REGISTRATION NUMBER:
                                                                                                   CLASSIFICATION:
                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                        ZIP:
                                                                                                                                                                                                                                                                                       STATE: MD
                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                    CITY: Rockville
                                                                                                                                                                                                                                                                                                               ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
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1171 MetapptysvalGluth:PhotomatglieValGlutysatgestYalGlutysatCyg 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAAC 360
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                                                                                                              16-SEP-1996
             A. Anders
                                                                                                                                                              Version #1.30
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176 156 96

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US-09-856-796B-1 (1-609) x US-08-710-324A-5 (1-198)
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
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                                                                                                                          US-09-411-657-5
                                                                                                                                                         RESULT 14
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 AMINO ACIDS
Sequence,5, Application US/09411657
Patent No. 6566328
GENERAL INFORMATION:
APPLICANT: Rosen, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: PROTEIN
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TYPE: AMINO ACID
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 ValTyrAspLeuLeuLysAspLeuGluGlyIleGlnThrLeuMetGlyArgLeuGlu 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              valGinPheLeuArgSerValPheAiaAsnSerLeuValTyrGlyAlaSerAspSerAsn 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGGGGGCCTCTGACAGCAAC 360
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                                                                                                                                                                                                                Glyphe 198
                                                                                                                                                                                                                                                                              GGCTTC 606
                                                                                                                                                                                                                                                                                                                               MetAspLysValGluThrPheLeuArgIleValGlnCysArgSerValGluGlySerCys 196
                                                                                                                                                                                                                                                                                                                                                                                                   ATGGACAAGGTCGAGACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGT 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerHisAsnAspAspAlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPhcArgLysAsp
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999.00
97.03%
97.03%
89.84%
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-856-796B-1 (1-609) x US-09-411-657-5 (1-198)
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pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDINE TYPE, PLOPPY disk
COMPUTER: IN PLOPPY disk
COMPUTER: IN PLOPPY DISK TO COMPUTED ON PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
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REGISTRATION NUMBER: 36,373
REGISTROPORT NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
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COMPUTER READABLE FORM:
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STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/411,657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: AMINO ACID
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                               181 ACCTCCCTCTGTTTCTCAAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAG 240
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                                                                                                                                                                                        301
                                                                                                                                                                                                                                                                                                             241 AAATCCAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGAGTGGAGCCC 300
                                                             361 GTCTATGACCTCCTAAAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAAGGCTGGAA 420
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                                                                                                                                                                                                                                         LysserAsnLeuGluLeuLeuArgileSerLeuLeuLeuIleGinSerTrpLeuGluPro 96
                                                                                                                                                                                                                                                                                                                                                                    ---SerLeuCysPheSerGluSerIleProThrProSerAsnArgGluGluThrGlnGln 76
                                                                                                                          LeuargalaHisargLeuHisGlnLeualapheaspThrTyrGlnGluphe----- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 AMINO ACIDS
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                              301-309-8439
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97.031
89.841
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Mismatches: Indels: Conservative

TCACACAACGATGACGCACTACTCAAGAACTACGGCTGCTGTACTGCTTCAGGGAAGGAC 540

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Alignment Scores:
Pred. No.:
                                                                    US-08-784-582-73
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US-08-784-582-73
                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/4/14.3000
INFORMATION POR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: anino acids
TYPE: anino acids
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APPLICANT: No. 6110707mington, Xarl D.
APPLICANT: No. 6110707mington, Xarl D.
APPLICANT: Clark, Samed, T.
APPLICANT: Thiggen, Anice E.
APPLICANT: Arade, Christian
APPLICANT: Madde, Christian
APPLICANT: Madair, Prod.
APPLICANT: Madair, Demnie
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Patent No. 6110707
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                                                                                                                                                                                                                                                                              APELICATION NIMBER: US 00/589,028
FILING DATE: 19-7M-1996
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION UNMERS: 37,642
REFERENCE/DOCKET NUMBER: UTSD:514
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,427
FILING DATE: 15-CCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/589,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTES: IBM POPPLY OF THE CONTROL OF THE COMPUTES: IBM POPPLY OF THE COMPUTED OF THE COMPUTED OF THE COMPUTED OF THE COMPUTED OF THE COMPUTED OF THE COMPUTED OF THE COMPUTED OF THE COMPUTED OF THE COMPUTED OF THE COMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MCGATTY, Dennis
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
TITLE OF INVENTION: SECRETORY CELL LINES
                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
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Houston
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                                                                                       linear
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Q	B	Ş	Db	ą	D	Q	В	Q	DЪ	Q	B	Q	Db	Q	Db	Ą	Db	Q	В	Q	-09-	Score: Percent Best Lo Query M	
556 ACATICCIGGGCATCGTGCAGTGCCGCTCT	181 AlaLeuLeuLysAsnTyrGly	496 GCACTACTCAAGAACTACGGG	161 ThrGlyGlnIlePheLysGln	436 ACTGGGCAGATCTTCAAGCAG	141 LysAspLeuGluGluGlyIle	376 AAGGACCTAGAGGAAGGCATC	121 SerValPheAlaAsnSerLeu	316 AGTGTCTTCGCCAACAGCCTG	101 LeuLeuArgIleSerLeuLeu	256 CIGCICCGCATCICCCIGCIC	81 SerGluSerIleProThrPro	196 TCAGAGTCTATTCCGACACCC	61 TyrileProLysGluGlnLys	172	41 LeuArgAlaHisArgLeuHi	121 CTCCGCGCCCATCGTCTGCA	21 LeuGlnGluGlySerAlaPh	61 CTTCAAGAGGGCAGTGCCTT	1 MetAlaThrGlySerArgTh	1 ATGGCTACAGGCTCCCGGACGTCCCTGCT	856-796B-1 (1-609) x US-08-7	926.50 int Similarity: 89.528 Local Similarity: 87.628 Match: 83.328	
GCCGCTCT 585		GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGA			LysAspLeuGluGlyIleGlmThrLeuMetGlyArgLeuGluAspGlySerProArg	ANGGNCCTAGAGGANGGCATCCANACGCTGATGGGGAGGCTGGANGATGGCAGCCCCCGG	SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu	AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA	LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg	CTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGGGGGGG	erGluSerlleProThrProSerAsnArgGluGluThrGlnGlnLysSerAsnLeuGlu	TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGANACACAA CAGAAATCCAACCTAGAG	TyrIleProLysGluGlnLysTyrSerPheLeuGlnAsnProGlnThrSerLeuCysPhe	AACCCCCAGACCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTC	LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPheGluGluAla	CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGGGGTTT	LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnAlaMet	CTTCAAGAGGGGAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT	MetAlaThrGlySerArgThrSerLouLeuLeuAlaPheGlyLouLeuCysLouProTrp	FICCCIGCICGGCTTTTGGCCTGCTCTGCCTGCCTGC	US-08-784-582-73 (1-360)	Matches: 184 Conservative: 4 Mismarches: 7 Indels: 15 Gaps: 1	
	200	555	180	195	160	435	140	375	120	315	100	255	80		60	171	0	120	20	60.			

Search completed: February 6, 2005, 13:29:08 Job time : 35 secs

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Score

US-09-853-688-2 US-09-853-688-4 US-10-788-318-2 US-10-788-318-4

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect
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seg length: 2000000000
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1: /cgn2_6/ptodata/2/pubpaa/US07
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US-10-621-693-73
US-10-621-693-693-73
US-10-621-693-693-73

sequence 2, Appli sequence 3, Appli sequence 3, Appli sequence 31, Appli sequence 51, Appli sequence 53, Appli sequence 53, Appli sequence 53, Appli sequence 53, Appli sequence 54, Appli sequence 54, Appli sequence 55, Appli sequence 57, Appli sequence 58, Appli sequence 58, Appli sequence 58, Appli sequence 58, Appli sequence 58, Appli sequence 58, Appli sequence 58, Appli sequence 58, Appli sequence 58, Appli

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Sequence 4, Appli Sequence 2, Appli Sequence 3, Appli Sequence 9, Appli Sequence 9, Appli Sequence 16, Appl Sequence 16, Appl Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 19, Appli

-853-688-2	
Nence 2, Application US/09853688	
ent No. US20020081605A1	
BRAL INFORMATION:	
PLICANT: COOPER, DAVID N.	
PLICANT: PROCTER, ANNIE M.	
PLICANT: MILLAR, DAVID S.	
TLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE WART.	HORMONE VART
TLE OF INVENTION: HUMANS, THE VARIATIONS AND THEIR USES	THEIR USES
TO VOLDENCE: MCM/8	
RRENT APPLICATION NUMBER: US/09/853,688	
RRENT FILING DATE: 2001-05-14	
MBER OF SEQ ID NOS: 66	
FTWARE: PatentIn Ver. 2.1	
ID NO 2	
ENGTH: 217	
YPE: PRT	
RGANISM: Homo sapiens	

ATTONS H

Result

US-09-853-688-2

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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Percent Similarity:
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SECTIONS: RELEATION (Sec. 2.1
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                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09853688
Patent No. US20020081605A1
                                                                                                                                                                                                       APPLICANT: PROCTER, ANNIE M.
APPLICANT: GREGORY, JOHN
                                                                                                                                                                                                                                                  APPLICANT: COOPER, DAVID N.
TYPE: PRT
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                    RESULT 3
                                                                                                                                            GENERAL INFORMATION:
APPLICANT: ARTICES PHARMACEUTICALS,
APPLICANT: HOUSTON Lou, L.
APPLICANT: SHERIDAN, Philip, J.
APPLICANT: HAWLEY, Stophen
APPLICANT: HAWLEY, Stophen
APPLICANT: TYPM TOWN THE
                                                                                                                                                                                                                                          Sequence 4, Application US/09969748C
Publication No. US20030161809A1
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           NEPLICANT, BASI, AMARTEM, TONES AND METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE
TITLE OF INVENTION, AGENTS ACROSS CELLULAR BARRIERS
FILE REFERENCE: 05722-013 TONESSET, DELICITAR BARRIERS
CURRENT, DEFLICATION MONBER, US/09/959,748C
                                                                                                             APPLICANT:
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GLYNN, Jacqueline, M.
CHAPIN, Steven
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, ORGANISM: Homo sapiens
US-09-969-748C-4
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PRICE APPLICATION NUMBER: US 60/248, 819
PRICE STUNG UNCE: USOC 11-13 60/244, 478
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SEQ ID NO 4
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US-09-856-796B-1 (1-609) x US-10-788-318-2 (1-217)
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Publication No. US20040137510A1
GENERAL INFORMATION:
APPLICANT: COOPER, DAVID N.
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US-10-788-318-4
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Publication No. US20040137510A1
GENERAL INFORMATION:
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CUEREST APPLICATION NUMBER: US/10/788,318
CUEREST FILING DATE: 2004-03-01
NUMBER OF SEG ID NOS: 62.1
SOFTMARE; SECENTIA Ver. 2.1
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APPLICANT: GREGORY, JOHN
APPLICANT: MILLAR, DAVID S.
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APPLICANT: PROCTER, ANNIE
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                                                                                                                                                                                LysAspLeuGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg
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                                                                                                                                                                                                                                                                                       AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA 375
                                                                                                                                                                                                                                                                                                                                            LeuLeuArgIleSerLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg 120
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161 ThrGlyGlnIlePheLyeGlnThrTyrSerLyePheAspThrAsnSerHisAsnAspAsp
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                                         ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAACTCACACAACGATGAC 495
                                                                                                                       AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG 435
                                                                                                                                                                SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 140
                                                                                                                                                                                                     AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA 375
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                                                                                  LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg
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US-09-856-796B-1 (1-609) x US-09-929-918-9 (1-217)
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SEQ ID NO 9
LENGTH: 217
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Patent No. US20020090678A1
                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 11
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PRIOR FILING DATE: 1999-05-25
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CURRENT FILING DATE: 2001-08-15
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APPLICANT: Slavchanco, 177m Wr.
APPLICANT: Ostanor, Olehandr
TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES
TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES
TILE REPRESENCE: PEDIAG. DOES.
                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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LENGTH: 217
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Patent No. US20020155100A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/804,4098
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 18
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APPLICANT: CHEUNG, ANTHONY T.
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ORGANISM: Homo
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                                               LysAspLeuGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg
                                                                                 AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG 435
                                                                                                                SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu
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                                                             121 CTCCGCGCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT------
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                                                                                                                                     CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCCTTATCCAGGCTTTTTTGACAACGCTAGT 120
                                            LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPheGluGluAla
                                                                                                             LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgProPheAspAsnAlaMet
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Hakes, David
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Zopf, David
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US-09-856-796B-1 (1-609) x US-10-411-037-48 (1-217)
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APPLICANT: Neose Technologies,
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Publication No. US20040043446A1
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
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BEZIOR FILLHG LARE: 2001.-0.10
BEZIOR APPLICATION NUMBER: US 66/344,692
BEZIOR EPILLHG LARE: 2001.-0.19
BEZIOR APPLICATION NUMBER: US 66/387,292
BEZIOR FILLNG LARE: 2002-66-07
BEZIOR FILLNG LARE: 2002-66-07
BEZIOR APPLICATION NUMBER: US 66/391,777
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APPLICANT: Bome, Caryn
ITTLE OF INVENTION: ALBERT GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF
EILE REFERENCE: GALACTOSIDASE A
EILE REFERENCE: GALACTOSIDASE A
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PRIOR APPLICATION NUMBER: US 60/407,527
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CURRENT FILING DATE: 2003-04-09
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APPLICANT: Neose Technologies,
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Publication No. US20040063911A1
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LENGTH: 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ROCKIN EMPONELING METHODS AND PROTEINS/PERTIOSS PRODUCED BY TITLE OF INVENTION; METHODS PROPERTY INVENTION; METHODS PLIZE REFERENCE: LOGISLOUS SES //D/KII.OS CORRENT FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING DATE: 2001-04-00 (1000) PRODE FILING PRODE FILING PRODE FILING PRODE FILING PRODE FILING PRODE FILING PRODE FILING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REICH APPLICATION NUMBER: US 60/391,777
REICH FILIMU BATE: 2020-266-25
REICH APPLICATION NUMBER: US 60/396,594
REICH APPLICATION NUMBER: US 60/404,249
REICH APPLICATION NUMBER: US 60/404,249
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PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
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GENERAL INFORMATION:
                                TITLE OF INVENTION: GRANICOVITE COLONY STRULATING PACTOR: REMORELING
TITLE OF INVENTION: GANCONOMINATION OF G-GSF
FILE REFERENCE: G04853-01-5054
CUMERAT APPLICATION NOMERS: UNI/10/10/52
UNDERST FILING DATE: MODIL-10-10-10/30,523
RECOR PELING DATE: MODIL-10-10-10/30,523
RECOR APPLICATION NOMERS: US 60/34/,592
RECOR APPLICATION NOMERS: US 60/34/,592
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APPLICATION

NUMBER: US 60/391,775

Chen, Xi Bowe, Caryn Bayer, Robert Hakes, David

Zopf, David DeFrees, Shawn Application US/10410962

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                                                                                            AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu
                                                                                                                          ThrGlyGlnIlePheLysGlnThrTyrSerLysPheAspThrAsnSerHisAsnAspAsp
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US-10-411-049-48

; Sequence 48, Application US/10411049

; Publication No. US20040082026A1
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LENGTH: 217
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PRICAR FILING DATE: 2002-06-25

PRICAR FILING DATE: 2002-07-17

PRICAR FILING DATE: 2002-08-18

PRICAR FILING DATE: 2002-08-18

PRICAR FILING DATE: 2002-08-28
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SOFTWARE: PatentIn version 3.2
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ORGANISM: Homo sapiens
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LeuLeuArgIleSerLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg CTGCTCCGGATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG SerGluSerIleProThrProSerAsnArgGluGluThrGlnGlnLysSerAsnLeuGlu TCAGAGTCTATTCCGACACCCTCCAACAGGGGGGAAACACAGAAACAGGAAATCCAACCTAGAG TyrIleProLysGluGlnLysTyrSerPheLeuGlnAsnProGlnThrSerLeuCysPhe CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT-----LeuGlnGluGlySerAlaPheProThrileProLeuSerArgProPheAspAsnAlaMet CTTCAAGAGGGCAGTGCCTTCCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT

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: SOUTWARE: Patentin version 3.2

; SEQ ID NO 48

; ELENGTH: 217

TYPE: PRT

; ORGANISM: Homo sapiens

US-10-411-049-48
                                 US-09-856-796B-1 (1-609) x US-10-411-049-48 (1-217)
                                                                         Percent Similarity:
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                                                                 Query Match:
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NUMBER OF SEQ ID NOS: 75
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
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TITLE OF INVENTION: ALPHA
                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 040853-01-5055
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
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Bayer, Robert
Hakes, David
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CURRENT PAPTLICATION NUMBER: 09/10/410-39 CURRENT PAPTLICATION NUMBER: 08/10/410-52 PAPTLM PAPTLICATION NUMBER: 08 6/10/45-52 PAPTLM PAPTLICATION NUMBER: 08 6/10/45-52 PAPTLM PAPTLICATION NUMBER: 08 6/10/4-52 PAPTLM PAPTLICATION NUMBER: 08 6/10/4-52 PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPTLM PAPT
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Bowe, Caryn
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Hakes, David
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Zopf, David
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                                                                                         RESULT 13
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SEQ ID NO 48
LENGTH: 217
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APPLICANT: DeFrees, Shawn
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/410,997
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                             NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version
                                                               PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
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Bowe, Caryn
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Hakes, David
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ORGANISM: Homo sapiens

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Best Local Similarity:
Query Match:
MPRICANT Notes Technologies, Inc.
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PRIOR FILING DATE: 2001-10-10	001-10-10	,523	
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FILING DATE:			
APPLICATION N	NUMBER: US 60/387, 292	. 292	
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APPLICATION N	NUMBER: US 60/391,777	,777	
PRIOR FILING DATE: 2			
APPLICATION N	NUMBER: US 60/396,594	.594	
	2002-07-17		
	APPLICATION NUMBER: US 60/404,249	,249	
	2002-08-16		
APPLICATION	NUMBER: US 60/407,527	,527	
ING DATE:	2002-08-28		
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TWARE:	ersion 3.2		
4			
LENGTH: 217			
ORGANISM: Homo sapiens	ene		
gnment Scores:			
1. No.:	7.52e-85	Length:	217
	1017.50	Matches:	200
cent Similarity:	92.17*	Conservative:	0
LOCAL SIMILARITY:	92.17%	Mismatches:	N
A MUCCHI	91.50%	Indels:	15
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US-09-856-796B-1 (1-609) x US-10-411-012-48 (1-217)

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121 376 141 436

316 AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGGACAGGTCTATGACCTCCTA

375

556 ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC

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RESULT 15
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Pred. No.:
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US-10-287-994-48
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RRIGE FILMS DATE: 2001-10-10

PRIOR FILMS DATE: 2001-10-19

RRIGE FILMS DATE: 2001-10-19

RRIGE FILMS DATE: 2001-10-19

RRIGE FILMS DATE: 2001-6-07

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Publication No. US20040137557A1
GENERAL INFORMATION:
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SEQ ID NO 48
LENGTH: 217
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APPLICANT; CHAK, XI
TITLE OF INVESTICN: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
TILE REFERENCE: 040653-01-5052-00
CURRENT APPLICATION NUMBER; UB/10/287,994
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PRICE RPILCATION NUMBER: US 60/396,594

PRICE FILING DATE: 2002-07-17

PRICE RPILCATION NUMBER: US 66/404,249

PRICE RPILCATION NUMBER: US 66/407,527

PRICE RPILCATION NUMBER: US 66/407,527

PRICE TILING DATE: 2002-08-28
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                                                                                                                                                                                                                                                                                                      61 TyrileProLysGluGlnLysTyrSerPheLeuGlnAsnProGinThrSerLeuCysPhe 80
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Bayer, Robert
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ORIGIN FEATURES

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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'db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
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cDNA encoding human growth factor 20K.
                                                                                                         Nakajimė, K. and Nagai, J.
RECOMBINANT PLASHID OF BECHERICHIA COLI FOR AMPLIFYING
RECOMPLEMENTANY DIA, OF HOMA GEOWITH HORMONE 20K
PALENT: JP 198524988-A 1 06-OCT-1986;
Patent: JP 198524988-A 1
                                                                                                                                                                 Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
Mammalla, Butheria, Friastes; Catarrhini; Hominidae; Homo.
1. (Gases 1 to 3387).
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29-MAR-1985 UP 198506208
MAKAJIMA KUNDO, NAGAI JUN
CINMIS/00//C12P21/02, (C12N15/00,C12R1:19);
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Pred. No. 1.5e-132;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                        ното вартеля
                                                                                                    Homo sapiens growth hormone 1, to
clone MGC:75439 IMAGE:30393581),
BC062475
                                                        Homo sapiens (human)
                                                                                    BC062475.1 GI:38566151
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Location/Qualifiers
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/mol_type="genomic RNA"
/db_xref="taxon:9606"
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100.0%; Pred. No. 1.4e-132;
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One 1, transcript variant 2, mRNA (cDNA
393581), complete cds.
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Direct Submission

Direct Submission

Submitted (17-NOV-2003) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genemics Office, National Cancer
Gene Collection (MCC), Cancer Genemics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Betheeda, MD 20832-2590, (bases 1 to 777)

CDNA Library Preparation: Invitrogen Corp CDNA Library Arrayed by: The I.M.A.G.B. Consortium DNA Sequencing by: Genome Sequence Centre, Email: cgapbs-remail.nih.gov Tissue Procurement: Dr. Michael Contact: MGC help desk NIH-MGC Project URL: http://mgc.nci.nih.gov Brownsteir

Serve Joine, Sarah Barber, Mabal Broom-John, Yaron Butterfiald, Andy Cham, Serve S. Chamid William Chowy, Aliano Choutier, Rath Andy Cham, Serve S. Chamid William Chowy, Aliano Choutier, Barb Cham, Sarah Cham, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca

Clone distribution: MCC clone distribution information can be foun through the I.M.A.G. Connertium/LIML str. http://lamge.llnl.gv. Bartis: IRM Flate: 141 Nov: p Column: 19
This clone was selected for full lamghs sequencing because it passed the following selection criteria: matched sman, gi: 20899251
Location/Dealliters Lound

organism="Homo sapiens"

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ORIGIN
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Bukaryoči Wateson, Choddata, Cranista, Vertebrata, Butoloostomi, Mammija, Butoli, Primates, Catarthini, Rominidae, Homo.

1 (bases, 1 C 1930). Primates, Catarthini, Rominidae, Homo.

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CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTATG 132

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GATGGCAGCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAA GATGGCAGCCCCCGGACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACACAAAC GTCTATCGCCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGAGGCTGGAA

55 492 GTCTATGACCTCCTAAAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAAGGCTGGAA 420 GTGCAGCTCCTCAGGAGCGTCTTCGCCAACAGCCTGGTGTATGGCGGCTCGGACAGCAAC 372 GTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAAC AMATCTAACCTMGAGCTGCTCCGCATCTCCTGCTGCTCATCCAGTCATGGCTGGAGGCCC AAATCCAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCC ACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAAACGCAGCAG ACCTCCCTCTGTTTTCTCAGAGTCTATTCCGACACCCCTCCAACAGGGAGGAAAAACACAACAG CTCCGCGCCCGTCGCCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTAACCCCCCAG CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTAACCCCCAG

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CTTCAAGAGGGCAGTGCCTTCCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT
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94.4%; Pred. No. 9.2e-120;
tive 0; Mismatches 34;
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Patent, Mo 018393-A 1 13-MOV-201;
University of Males College of Medicine (GB)
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Sequence 1 from Patent W00185993.
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                 ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAAACGATGAC
                                                                     AAGGACCTAGAGGAAQGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG
                                                                                          AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG
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ACTOGGCAGATCTTCAAGCAGCCTACAGCAAGTTCGACACAAACTCACACACGATGAC
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/mol_type="unassigned DNA"
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*436 ACTOGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACCATGAC
531 ACTOGGCAGATCTTCAAGCAGACCTACAGCACAAGTTCGACACAAACTTACACAACCATGAC
531 ACTOGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACAACCATGAC
                                                                  471
                                                                                                     376
                                                                                                                                    411
                                                                                                                                                                       316
                                                                                                                                                                                                      351
                                                                                                                                                                                                                           256 CTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTTGGAGCCCGTTGCAGTTCCTCAGG
                                                                                                                                                                                                                                                                            291
                                                                                                                                                                                                                                                                                                     196 TCAGAGTCTATTCCGACACCGTCCAACAGGGAAACACAACAACAGAAATCCAACCTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                             171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTTGACAACGCTAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent: WO 0136635-A 25 25-MAY-2001;
Curagen Corporation (US)
Location/Qualifiers
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Neurite outgrowth-promoting factor homologue and nucleic acids
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Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.
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Sequence 25 from Patent W00136635.
XX149376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                      CTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG
                                                              AMOGACCTAGAGGAMGGCATCCMANCGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG
                                                                                                 AAGGACCTAGAGGMAGGCATCCAAACGCTGATGGGGAGGCTGGMAGATGGCAGCCCCCGG
                                                                                                                                    AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA
                                                                                                                                                                                                                                                                         TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAACCTAGAG
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                                                                                                                                                         AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA
                                                                                                                                                                                                                                                                                                                                                                                                          CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGAAGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCCGCGCCCATCGTCTGCACCAGCTTTTGACACCACCTACCAGGAGTTT------
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/mol_type="unassigned DN
/db_xref="taxon:9606"
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Pred. No. 1.3e-119;
0; Mismatches 0;
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Length Indels

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Gaps

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540

470

410 315 350 255 290 195 230 171 170 120 60

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VERSION
KEYWORDS
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Best Local Similarity
Matches 609; Conserv
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591 GCACTACTENAGAACTACGGGCTGTCTACTGCTTCNGGACXTGGACNAGGTCGAG 650
                                                                         471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGGCTACAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGGCCTGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent: WO 0136635-A 30 25-MAY-2001,
Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Majumder, K., Prayaga, S.K. and Burgess, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AX149381
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                                  ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACGATGAC 495
                                                                         AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGGAGGCTGGAAGATGGCAGCCCCCGG
                                                                                                                AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAAGGCTGGAAGATGGCAGCCCCCGG
                                                                                                                                                   AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA
                                                                                                                                                                                      AGIGICITICGCCAACAGCCIGGIGIACGGCGCCTCTGACAGCAACGICIAIGACCICCIA 379
                                                                                                                                                                                                                             CTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG
                                                                                                                                                                                                                                                                CTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG
                                                                                                                                                                                                                                                                                                       TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAACCTAGAG
                                                                                                                                                                                                                                                                                                                                          TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAACCTAGAG
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ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 1.3e-119;
0; Mismatches 0;
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Best Local Similarity
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TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAACCTAGAG

653 593 195 173 473 120 413

121 CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT------61 CITCAAGAGGGCAGIGCCITCCCAACCATTCCCITATCCAGGCTTTTTTGACAACGCTAGI

Conservative

0; Mismatches Score 554; DB 6; Length 3477; Pred. No. 1.1e-119;

Indels 45;

Gaps

93.1%;

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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nokajima, K. and Nagai, J.
RECOMBINANT PLASMID OF ESCHERICHIA COLI
GROWTH HORNONE COMPLEYENSWIARY STRAND DNA
PRICHI: JP 1986202689-A 1 08-SEP-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthetic construct
synthetic construct
other sequences, artificial sequences
1 (bases 1 to 3477)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E00952 3477 bp DNA linear PAT 29-SEP-1997 Plasmid DNA for amplifying human growth factor gene in E.coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAKAJIMA KUNIO
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                                                                                                                                                                                                                                                                                                                                                                                                                              Artificial gene
Artificial sequence; Genes
JP 1986202689-A/1
                                                                                                                                misc_feature
                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                      topology: Linear;
hypothetical: No;
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                                                                                                                                                                                                                                                    anti-sense: No;
                                                                                                                                                                                                                                                                                                                    strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                  NAKAJIMA KUNIO, NAGAI JUN
                                                                                                                                                                                                                                                                                                                                                                                         04-MAR-1985 JP 1985042404
organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"
                                                                1. .3477
                                                                                       Location/Qualifiers
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                                                                                                                                                            /note='G=(G)n'
                                                                                                                   /note='A=(A)n'
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Best Local Similarity 95.7%;
Matches 583; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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Sequence 7
CQ827137
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Mammalia; Butheria; Primates; Catarrhini; Hominidae;
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                                      AAATCCAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTGCTCATCCAGTCGTGGTGGAGGCC 300
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/db_xref="taxon:9606"
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Pred. No. 1.4e-119;
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AAATGGAACCTAGAGCTGCTCCGCATCTCCCTGCTCATCCAGTCGTGGAGCCC ACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAACGCAGCAG ACCTCCCTCTGTTTCTCAGAGTCTATTCCGACACCCTCCAACAGGGAGAGAACAGAACAG CTCCGCGCCGTCGCCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTAACCCCCAG CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTAACCCCCAG CTTCAMGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGCCTTTTTGACAACGCTAGT

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                                                                 Query Match 90.8%; Score 553; DB 6; Best Local Similarity 94.3%; Pred. No. 2.2e-119; Matches 574; Conservative 0; Mismatches 35;
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Patent: WO 02101002-A 5 19-DEC-2002;
GenOdyssee (FR)
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AX659150:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ATGGCTGCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTTGGCCTGCTCTGACTGTCCTGG
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/mol_type="unassigned DN
/db_xref="taxon:9606"
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Patent: EP 1295938-A 5 26-MAR-2003;
GenOdyssee (FR)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GTGCAGTTCCTCAGGAGTCTTTOGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAAC
                                   AAATCTAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCC
                                                          ACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAACGCAGCAG
                                                                                                       ACCTCCCTCTGTTTCTCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAG
                                                                                                                                                         CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTAACCCCCAG 180
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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Pred. No. 2.2e-119;
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                                                            AAATCCAACCTAGAGCTGCTCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCC
                                                                           AMTCCMACCTAGAGCTGCTCCGCATCTCCCTGCTGCTGATCCAGTCGTGGTGGTGGAGCCC 300
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421 GATGGCAGCCCCCGGACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAAC 480
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                                                                                                                                                                Fagan, R.J., Pholip C.B., Rodrigues T.M., Yorke, M. and de Tiani, M. 
Splice variant & the haman pluttary growth homeone 
Patent: NO 004050704. 25 17-UN-2004; 
ARSS TRADING S.A. (QNJ. A.25 17-UN-2004; 
LOCKLIGHT QUALIFIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 25 from Patent
CQ827155
CQ827155.1 GI:49455732
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                                                                                                            CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT 120
CTCCGCGCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT-----
                              CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTAACCCCCAG 180
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 5.8e-119;
0; Mismatches 18;
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90.4; Score 550.9; DB 6; Length 654; 11 Smilarity 92.88; Pred Mo 7, 7:e-112; 607; Comervative 0; Mismatches 2; Indels 45; Gaps 1;	TREER: NO CONSIDER AND A 12-ANY-2003; OR CONSIDER AND A 12-AN	KEROR SEPLEME (Inman) KEROR SEPLEME (Inm.) KEROR SEPLEME (Inm.) KEROR SEPLEME (INC.) KEROR SEPLEME (INC.) KEROR SEPLEME (INC.) KEROR SEPLEMENT (NY166633 from Parent 0033042408. DNA linear PNT 25-UDK-2003 ANY36633 disagraphy 0033042408.	ACATTOCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGGAGCTGTGGCTTCTAG 609	96 GASTACTEMBANCTACGGGCTGCTCTÄCTGCTTCAGGAAGGACATGGACAAGGTCGAG 555	495 495 ACTGGGCHARTTTCANGCHACCTROHOCOMOTTCGACHARTTCHCHCHATGATCHC 495 491 ACTGGGCHARTCTCANGCHACCTROHOCOMOTTCGACHARACTCHCHCHATGACTHAC 491 ACTGGGCHARTCTCANGCHACCTROHOCOMOTTCGACHACHACTCHCHCHACGATGAC 540	376 ANGENCTANGGANGGCATCANACGCTRATOGGCAGGTGSANGATGGCAGCCCCCGG 435 421 ANGENCTANGGANGGCATCCANACGCTRATOGGCAGGTGSANGATGGCAGCCCCCCGG 480	316 AGTOTOTTOGCOMACHGCTGGTGTACGGGGCCTCTGMACAGCMACGTCTMTGACCTCCTM, 375



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Database :
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Maximum Match 100%
Listing first 45 summaries
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Panel Social Control of	AAN82235		528	85.9	523.2
Add17918 Pusion pr	ADG17918		699	86.2	525
Add17919 Fusion or	ADG17919	10	681	86.2	220
Aaf83835 Human PCT	AAF83835	٠	812	86.5	526.8
Add Bass Human Sup	ADQ38455	13	1495	87.2	530.8
Aav60639 Human gro	AAV60639		663	88.1	536.4
Add38479 Human SNP	ADQ38479	13	1043	88.4	538.2
Adn81286 DNA encod	AAN81286	,	651	88.4	538.2
Add38475 Human SNP	ADQ38475	13	1443	88.5	539.2
Mal59998 Himan oro	AL59998	9	821	89.0	541.8
Aan71219 Semience	AAN71239	Ė	651	89.4	544.6
	ADQ38457	13	1497	89.5	544.8
Abx14644 DNA encod	ABX14644	10	651	89.7	546.2
Adle0072 Human gro	AAL60072	9	821	89.9	547.2
	AAQ04700	N	814	90.2	549.2
	ADN49719		799	90.2	549.2
Himan	ACC78890		799	90.2	549.2
Human.	AAC86395		799	90.2	549.2
	AAD17490		799	90.2	549.2
Himan group	AAL46250		769	90.2	549.2
Adm32918 Nicleotid	ADM32918	12	654	90.2	549.2

31 28 28 28

AAA46696

AAA46696 standard, DNA; 609 ВP

AAA46696;

25-SEP-2000 (first entry)

DNA encoding a human growth hormone (hGH).

Rimanı growth hormone; höd; inhibitor, nuclear factor-keppaB, NF-kappaB, maliti-drug resistance gene, malignant hempathy, solid tumour; malignant blood disease; leukaemis; lymphoms, golid cancer; ds.

Homo sapiens

/*tag= Location/Qualifiers 1. .609

/product= "growth hormone"

W0200030587-A2.

24-NOV-1999; 02-JUN-2000. 99WO-FR002897.

25-NOV-1998; 98FR-00014858

(CNRS) CENT NAT RECH SCI

Hirsch F, Haeffner A;

WPI; 2000-399901/34. P-PSDB, AAY93637

Treatment of hematological or solid tumors using an inhibitor of the artesian of nuclear factor-kapaB, particularly to prevent development of resistance to chemotherapeutics.

Claim 4; Page 26-27; 30pp; French

AAN60678

The present sequence encodes a human growth hormone (hGH). The human

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$88888888
                                                                                                                                                                             ADQ38456
ID ADQ
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              Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human; gene; ds.
                                                              Human SNP containing myocardial infarction-associated gene, SEQ ID 119
                                                                                                           18-NOV-2004
                                                                                                                                            ADQ38456;
                                                                                                                                                                             ADQ38456 standard; DNA;
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Pred. No. 7e-140;
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20-DEC-2002; 2002US-0434778P
10-MAR-2003; 2003US-0453135P
30-APR-2003; 2003US-0466412P
23-SEP-2003; 2003US-0504955P
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the individual's nucleic acids.
                        identifying an individual
myocardial infarction by or
                                                                                    P-PSDB; ADQ39284
                                                                                                                                         Cargill M,
                                                                                                                                                                                 (APPL-) APPLERA CORP
                                                                                                                                             Devlin JJ,
                                                                                                                                                 Iakoubova
                        who has an altered risk for developing detecting a single nucleotide polymorphism in
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Claim 7; SEQ ID NO 119; 145pp; English. invention relates to a novel method for identifying an individual who

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Sequence 1354 BP; 284 A; 396 C; 344 G; 309 T; 0 U; 21 Other;

Ś В Matches 593; Query Match Best Local Similarity 117 19 ATGGCTRCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCCTGG ATGGCTACAGGCTCCCGGACGTCCCTGCTCCTGGCCTTTTGGCCTGCCCTGCCCTGG CTTCAAGAGGGCAGTGCCTTCCCAACGATTCCCTTATCCAGGCTTTTTGACAAACGCTAGT 120 Conservative 98.5%; 14; Mismatches Score 599.8; DB 13 Pred. No. 1.5e-137; DB 13; Indels Length 1354 ٥, Gaps

176

ACCTCCCTCTGTTTCTCAGAGTCTATTCCGACACCCTCCAACAGGGAAACACAACAACA CTTCAAGAGGGCAGTGCCTTCCCMAACCATTCCCTTATCCAGGCTTTTTGACAACGCTATG CTCCGCCCCATCGTCTGCACCAGCTGGCMTwTGACACCTACCAGGAGTTTAACCCCCAG CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTAACCCCCAG 180 236 240 296

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ADQ38467
ID ADQ3
Identifying an individual who has an altered risk for developing myocardial infaction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                                       WPI; 2004-533949/51.
P-PSDB; ADQ39295.
                                                                                                                       Cargill M,
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10-MAR-2003; 2003US-0453135p.
30-APR-2003; 2003US-0466412p.
23-SEP-2003; 2003US-0504955p.
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                                                                                                                                                                                                                                                                                                                                                                            HOMO Sapiens
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                                                                                                                                                         (APPL-) APPLERA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      containing myocardial infarction-associated gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                    detection; single nucleotide polymorphism; SNP
                                                                                                                       Iakoubova
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Claim 7; SEQ ID NO 130; 145pp; English

invention relates to a novel method for identifying an individual an altered risk for developing myocardial infarction. The method

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ATGGACAAGGTCGAGACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGT

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GGCTTCTAG 609

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GECTTCTAG

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The invention described a method of describs variation in growth hormone (cd) ((dd)), and these one of describs variation in growth hormone (cd) ((dd)), and these one of the service of the service of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting growth hormone variants (GH1), useful in screening patients growth hormone irregularities, comprises comparing the nucleotide sequence of a GH1 gene from a test sample with that of a standard sequence of the human GH1.
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14-JUL-2000; 2000BP-00306004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostic tests for inherited GH deficiency.
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   GCACTACTCAMGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCGAG
                                                                                                          ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC
                                                                                                                                                                                       AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG
                                                                                                                                                                                                                             AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA
                                                                                                                                                                                                                                                        AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA
                                                                                                                                                                                                                                                                                                      CTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG
                                                                                                                                                                                                                                                                                                                                CTGCTCGGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG
                                                                                                                                                                                                                                                                                                                                                                              TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACACAGAAATCCAACCTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAACCTAGAG
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                                                                            ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC
                                                                                                                                                    AAGGACCTAGAGGAAGGCATCCAMACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 554;
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AAS18888 standard; DNA; 654

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ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG

DNA encoding 12-MAR-2002 growth hormone 1 gene (first entry) (GH1), E56G mutant

82222222222 Growth hormone 1; GHz; onteopathic; genne therapy; protein therapy; disheres, obsetty; infection acromapaly; jointime; oodium retention; satety retention; metabolic myndrome; mood disporder; sleep disporder; octoch hormone deputanction; demilial growth hormone deficiency; short seauure; pituitery sicrege defect; human; mutant; da.

Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting growth hormone variants (GH1), useful in screening patients growth hormone irregularities, comprises comparing the nucleotide sequence of a GH1 gene from a test sample with that of a standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 7; 95pp; English
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/note= "Growth hormone 1 mutant E56G"
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ABK81192 ID ABK ABK81192 standard, cDNA, 821

ВP

(first entry)

cDNA encoding human growth hormone

Treasses lular transport, transcytotic transport, paracellular trans-respiratory system disorder; lung cancer; tumour, asthma; pathogonic infection; allergy-related disorder; gastrointestinal tract disorder; gastrointestinal hormone disorder; paracellular transport,

Chron's disease, eating disorder; polyimmunoglobulin receptor;

Homo sapiens

W0200228408-A2

02-OCT-2001;

2001WO-US030832

13-NOV-2000; 14-NOV-2000; 02-OCT-2000; 2000US-0237929p. 2000US-0248478p. 2000US-0248819p. 2001US-0267601p.

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CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCCTTATCCAGGCTTTTTGACAACGCTAGT

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Houston F Sheridan PJ, Hawley S, Glynn JM, Chapin S,

Basu

WPI, 2002-416628/44

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 22, 379pp, English.
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GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAAGGACATGGACAAGGTCGAG
                                                                                                                                                ACTOGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC 601
                                                                                                                                                                                                               ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC
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Pred. No. 2.5e-126;
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Pagan RJ, (ARES-) ARES TRADING 05-DEC-2002; 2002GB-00028441 05-DEC-2003; 2003WO-GB005295

Phelps CB,

Rodrigues TM,

Yorke M,

De Tiani

WPI; 2004-450722/42

Claim 9, SEQ ID NO 7, 83pp; English bacterial and parasitic infections

Novel INSP101 polypeptides or fragments useful for treating Cushing's disease, endocrine disorders, cell proliferative disorders, cachexia,

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556

ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG 609

495 541 483 421 361

The immention relates to a polyapptide (i) computating a fully defined to applying adjunct of 190 of 19 mine acids (ii). Lie frequent functional graph in a graph of the property of the prope

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Best Local :
Matches 58:
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                                          ATGGACAAGGTCGAGACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGT
                                                                                     ATGGACAAGGTCGAGACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGT
                                                                                                                                                                                                                                                                                                     GATGGCAGCCCCCGGACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAAC
GCCTTCTAG 609
                                                                                                                                                                                                GATGGCAGCCCCCGGACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAAC
                                                                                                                                                                                                                                                                                                                                                           GTCTATGACCTCCTANAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                GTCTATGACCTCCTAAAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 553.8; DB 12
Pred. No. 2.6e-126;
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/product=

Location/Qualifiers "PGH isoform"

phallic growth; hypochondropiata; cognitive function; arteriopicecosis; esmocrimera destines; menta textdetion; intentin resistance; tumour; pp; II disbetes; hemacloigical disorder; aucoimane disease; altergy; infectious disease; metholic disease; altergy; infectious disease; metholic disease; altergy; infectious disease; metholic disease; altergy; infectious disease; metholic disease; see altergy; infectious disease; per metholic disease; per disease; foetal ammipholicy; gent release; supplication; see altergation; altergation; see altergation

Human, growth hormone-V; hGH-V, craniofacial

development, anglogenesis,

growth hormone (hGH)-V isoform 4 DNA

cancer; placental growth hormone;

gene; de

gapiens.

2222

WPI, 2003-148787/14 Escary J; (GENO-)

AAE33559. GENODYSSEE 07-JUN-2001; 21-SEP-2001; 27-SEP-2001;

2001US-0296149P 2001EP-00402435 2001US-0325401P

07-JUN-2002; 2002WO-EP008919

W02002101002-A2 variation mat_peptide Variation sig_peptide

79. .606 /*tag= d

/standard_name=

"Single nucleotide polymorphism"

/*tag= c /product= "Mature F replace(409,G) /*tag= e /*tag= e

PGH isoform'

standard_name= "Single nucleotide polymorphism"

Or The invention relates to human growth hormone (tob) vy gene polypections of an objection relates sequences of the invention are useful for preventing the many states of the prevention are useful for preventing the many states of the prevention diseases Wew polymucleotide derived from the nucleotide sequence of the human growth hormonary gene, useful for preparing a sedicement for preventing or treating a disease or disorder, e.g. mental retardation, autoimmune 8 or cancers. 65; 35pp; English

XXX888888888888888888888888888888

RESULT 8 AAD51435 ID AAD5 XX

AAD51435

standard; DNA; 609

GGCTTCTAG 600

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease e.g. feetal abnormalities such as feetal ansujaddy. The invention is also useful in gene therapy. The present sequence i isoform DNA. hGH-V gene codes for placental growth hormone (PGH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 609 BP; 131 A; 192 C; 154 G; 132 T; 0 U; 0 Other;
                                       Human SNP containing myocardial infarction-associated gene, SEQ ID 151
                                                                    18-NOV-2004
                                                                                                                   ADQ38488 standard; DNA; 855 BP
         cardiant; gene therapy; human; gene; ds.
                      Myocardial infarction; detection; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTTCANGAGGGCAGTGCCTTCCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTATG
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                                                                                                                                                                                                                            ATGGACAAGGTCGAGACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGT
                                                                                                                                                                                                                                             ATGGACAAGGTCGAGACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGT
                                                                                                                                                                                                                                                                           GATGGCAGCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAAA
                                                                                                                                                                                                                                                                                                                                             GTCTATCGCCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGAGGCTGGAA
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                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 4.1e-126;
0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 609.
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10-MAR-2003;
30-APR-2003;
23-SEP-2003;
Cargill M, Devlin JJ.
                            (APPL-) APPLERA CORP.
                                                                                                        20-DEC-2002,
                                                                                                                                        22-DEC-2003;
                                                            2003US-0434778P.
2003US-0453135P.
2003US-0466412P.
2003US-0504955P.
                                                                                                                                        2003WO-US040978
   Takoubova O;
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P-PSDB; ADQ39316 WPI; 2004-533949/51

Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism the individual's nucleic acids. ä

Claim 7; SEQ ID NO 151; 145pp; English.

relates to a novel method for identifying an individual who

Live investigate control of the properties of the product of the control of the c

Matches 573; Query Match Best Local Similarity Sequence 855 BP; 192 A; 267 C; 219 G; 170 T; 0 U; 7 Other 142 ATGGCTGCAGGCTCCCGGACGTCCTGCTTCCTGGCTTTTTGGCCTGCTCTGCCTGTCCTGG Conservative 94.11; 90.7%; 1; Mismatches Pred. No. 5.6e-126; Score 552.6; DB 13; Indels Length 855, 0,

0

181 262 202 121 CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTGACACCTACCAGGAGTTTTAACCCCCCAG CTCCGCGCCCGTCGCCTGTACCAGCTGGCATATGACACCTATCAGGAGTTRAACCCCCAG CTTCAAGAGGGCAGTGCCTTCCCCAACCATTCCCCTTATCCAGGCTTTTTGACAACGCTATG

321 180 261 201

61 CTICAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTTGACAACGCTAGT 120

322 ACCTCCCTCTGCTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAAACGCAGCAG ACCTCCCTCTGTTTCTCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAG 383 240

AAATCCAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTGATCCAGTCGTGGCTGGAGCCC

300

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241

WO2004058052-A2. 15-JUL-2004. .

Homo sapiens.

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PT CDS	1 A MASA MANAGET COCCUMA CORFECT PROCESS TO TRANSCORPE CONTROL OF THE MANAGEMENT OF
XX Homo	
	Sequence 3557 BP; 927 A; 902 C; 897 G; 831 T; 0 U; 0 Other;
KW Cush	Gweetle ze derived trom human pitutisary gland tissue, and allows pro- greeistance mose, the produced by a circular plasmid carrying a namp resistance mose, the produced by a circular plasmid carrying a namp ampicillin containing medium. See also SIGIROSSON
	Disclosure; Table 1-9; 9pp; Japanese.
	Plasmid for amplification of human growth hormone gene - derived from human pituitary gland tissue.
XX ds;	WPI; 1986-276387/42.
	(MAKA/) NAKAJIMA K.
	04-MAR-1985; 85JP-00042404.
	04-MAR-1985; 85JP-00042404.
ADP43297	08-SEP-1986.
RESULT 1	JP61202689-A.
Db	Homo sapiens.
QY	Pituitary gland; E.coli; dg.
Db	Human pro-growth hormone,
Ą	24-OCT-1991 (first entry)
Db	AAM60801;
S	AAN60801 standard; DNA; 3557 BP.
B	0801 0001
Ş	
D	742 GGTTTTTAG 750
Q	3 8
. D	541 ATGGACAAGGTCGAGACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGT 600
Q	
₽ :	
ę	562 GATGGCAGCCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAA 621
₽ \$	
? 8	502 GTCTATCGCCACCTGAAGGACCTAGAGGGATCCAAACGCTGATCTGGAGGCTGGAA 561
3 5	
₽,	442 GTGCAGCTCCTCAGGAGCGCTCTTCGCCAAACACCTGTGTGTG
Q	381 GTGGAGTTCTTCAGAACTGCTCGGCATCTCCCTGCTGCTCATCCAGTCAATGGCTGGAAGCCC 441

994	934	496	874	436	376	754	316	694	256	196	574	172	514	121	454	_
AGATTCTTGGGATCGTGAATGCGGTCTGTGGAGGGAGCTTGTGGTTCTNG 609 ACATTCCTGGGATCGTGCAGTGCCGCTTGTGGAGGGAAGCTGTGGCTTCTNG 1047	GCACTACTCNAGAACTNCGGGCTGCTCTACTGCTTCNGGAAQGACATGGACNAGGTCGAG	GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGA	* ACTROGERGATETECAAGEAGACATACAGEAAGTTCGACACAAACTCACACAACAACTACAGCAAGTTCGACACAAACTCACACAACAACTACAGCAAGTTCGACACAAACTCACACAACAACTACAACA	ACTOSGCAGATCTTCAAGCAGACCTTACAGCAACTTTCCAAGATCGCAAGATCGCAGCCCCCGG	6 AAGSACCTRGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG 435	AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGGAACGTCTATGACCTCCTA	AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA	4 CTGCTCCGCATCTCCTCATCCAGTCGTGGCTGGAGTCCCTCAGG 753	ALAMANTICIATTICCGACROCOTOCAACAGGAGAACAGAACAGAACAGAACCTÁGAG CTACTOCACATTOTOCOTOCATAGAGTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTO	TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACACAACAGAAATCCAACCTAGAG	TATATCCCAAAGGAACAGAAGTATTCATTCCTGCAGAACCCCCAGACCTCCCCTCTGTTTC	- AACCCCAAGACCTCCCTCTTTTC	CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGAAGAAGCC	CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT	CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT	61 CTTCAAGAGGGCAGTGCCTTCCCAAGCATTCCCTTATCCAGGCTTTTTGACAAGGCTAGT 120

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ADP43297 standard; DNA, 677 BP.

09-SEP-2004 (first entry) ADP43297;

Human pituitary growth hormone variant INSP101 cloned gene.

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lomo sapiens

Mat

Location/Qualifiers 34. .651

/product= "human oituitary growth hormone variant INSP101 with C-terminal His tag"

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The invention relates to a physpitch (1) comprising a fully defined as a growth horson, which are the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the composite of the compos
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                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel INSP101 polypeptides or fragmente useful for treating disease, endocrine disorders, cell proliferative disorders, bacterial and parastic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-450722/42.
P-PSDB; ADP43298.
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 677 BP; 157 A; 210 C; 167 G; 143 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                            61
                                                                                                                                                                               CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTAACCCCCAG 180
                                                                             CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTATG
                                                                                                                            CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAAACGCTAGT
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                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                95.6%;
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                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                       Score 551.2; DB 12;
Pred. No. 1.2e-125;
O; Mismatches 18;
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                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
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                               (MAXY-) MAXYGEN APS.
(MAXY-) MAXYGEN HOLDINGS LTD.
                                                                                                  11-JAN-2001; 2001DK-00000042.
11-JAN-2001; 2001US-0261411P.
                                                                                                                                                                               10-JAN-2002; 2002WO-DK000017
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ABK90830 standard; DNA; 654 BP
                                                                                                                                                                                                                                                                                               Human; growth hormone; häl; Turner's syndrome; achondroplasia;
growth hormone deticiency in adults; ofDha; chronic renal insufficiency;
renal failure in children; acquired immune deficiency syndrome; AIDS;
renal failure in
                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding human growth hormone (hGH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT------
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note: "Mature human growth hormone"
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ACTOGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAAGGATGAC
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61 CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTTGACAACGCTAGT

120 60 60

 Best Local Similarity Matches 607; Conserva Query Match

Conservative

90.4%;

Score 550.8; DB 10; Length 654; Pred. No. 1.5e-125; 0; Mismatches 2; Indels 45;

Gaps

Sequence 654 BP; 150 A; 207 C; 160 G; 137 T; 0 U; 0 Other

The present invention relates to a method for detecting a variation in plutiary expressed competition (will affective to fact sean indicator competing the menumon deviated for at an indicator competing the menumon deviated for at an individual. The method competes expense of the human Goll point. The present expressed in the coding and the competing an

Detecting a variation in pituitary-expressed growth hormone (GHI) useful as an indicator of growth hormone (GH) Varianction comprises comparing the sequence obtained from the test sample with a standard sequence of the human GHI gene.

P-PSDB; ADC61299 WPI; 2003-449578/42 Cooper DN (UYWA-) UNIV WALES COLLEGE OF MEDICINE 12-NOV-2002, 2002WO-GB005103 22-MAY-2003 W02003042408-A2

Procter 2001GB-00027213

AM, Gregory J, Millar DS;

Claim 1, Fig 6; 70pp, English

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ADC61349
ID ADC6
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                                                                                                Growth Hormone; GH1; human;
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product= "Human growth hormone,
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RESULT 14
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antimicrobial; cardiant; gene therapy; chromosome 17q;
single nucleotide polymorphism; gene; 88.
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12-NOV-2001; 2001GB-00027214.
14-NOV-2001; 2001GB-00027328.
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Best Local Similarity
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nucleic acid sequence, GH1, useful for disgnosing or
diabetes, infection, cancer or cardiac conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             In present sequence is the octing sequence of the human growth hormous 
out pees the invention relates to anturally-occurring matching less 
100546/4) that have been desceted in a cobort of patients with mbort 
sectors. Nethods are provided for descetion have writants, for sersening 
patients for growth hormous trespilatities, and for producing variant 
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92.8%; Pred. No. 1.5e-125;
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4	601 ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG 654	601	₽
9	ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG 609	556	á
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GAC 495	ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC	436	ş
CGG 480	LAAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCC	421	문
CGG 435	376 AAGGACCTAGAGGAAAGGCATCCAAACGCTGATGGGAAGGCTGGAAGATGGCAGCCCCCGG 435	376	S
CTA 420	361 AGTGTCTTCGGCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA 420	361	밁
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                                        Matches 607; Conservative
                                                        Query Match
Best Local Similarity
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Patent No. 6410220
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 5594 base pairs
                                                                                                                                    MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MUSTING, ANN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 26-Aug-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 55401
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NATURE TECHNOLOGY CORPORATION, TITLE OF INVENTION: SELF-ASSEMBLING GENES, THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            434.8
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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COMPUTER: IBM PC COMPACTIVE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 119 NORTH FOURTH STREET, SUITE 203
                                                                                                                                                                                                                                                                                                TELEFAX: 612-305-1228
                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US98/03918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/380,190A
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US-09-949-016-2791
US-09-949-016-2792
US-09-949-016-2793
US-09-949-016-2793
US-08-388-2670-1
US-09-277-720-1
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US-08-710-324A-3

US-09-411-657-3

US-09-827-688-13
                                    0; Mismatches
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PCT-US93-09232-1
                                                        Score 550.8; DB 3;
Pred. No. 3.4e-153;
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Patent No. 6410220
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: MUETING, RAASCH & GEBHARDT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL
TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2810
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                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                              APPLICATION NUMBER: PCT/US98/03918
FILING DATE: 28-FEB-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 5540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
GUARRE. ASSESSMENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: MINNESOTA
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US-09-284-878-2

Sequence 2, Application US/09284878 Patent No. 6342375 GENERAL INFORMATION:

APPLICANT: APPLICANT: APPLICANT:

Olazaran, Martha Guerrero Saldana, Hugo Barrera Salvado, Jose Maria Viader

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US-09-380-190A-21
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
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                                                556 ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG 609
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TELEPAX: 612-305-1228
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Pred. No. 3.8e-153;
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RESULT 4
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LENGTH: 663
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PRIOR APPLICATION NUMBER: PCT/MX97/00033

REOR FILING DATE: 1997-10-24

NUMBER OF SEQ ID NOS: 9

OSFWARE: Patentin Vet. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEATURE:
OTHER IMPORMATION: Description of Artificial Sequence: DNA encoding
OTHER IMPORMATION: the meture human growth hormone, containing an
OTHER IMPORMATION artificial basi site introduced by modifying
OTHER IMPORMATION; nucleotides at positions 21 and 24
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CURRENT PPELICATION NUMBER: US/09/284,878
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Pred. No. 1e-1
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RESULT 5
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TILE REPRENCIS CADATON

CHEST APPLICATION NUMBER: US/07949.016

RECOM APPLICATION NUMBER: US/0744.55

RECOM APPLICATION NUMBER: US/0747.56

RECOM APPLICATION NUMBER: US/0747.68

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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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Best Local :
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ORGANISM: Human
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Pred. No. 1.9e-149;
0; Mismatches 2;
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Application

US/09949014

Patent No. 6812339

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Matches 605; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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CURRENT APPLICATION NUMBER: US/09/949,016
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                                        ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG 609
                                                                                          GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGGGAAGGACATGGACAAGGTCGAG
                                                                                                                          ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC
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92.5%;
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Pred. No. 1.9e-149;
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; TYPE: DNA
; ORGANISM: Humar
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Retent No. 6311339

GREEN, MINOCATTEN, CALS of tal.

TITLE OF INVESTION FORWARDEDS 11 KNOWN CHAIS ASSOCIATED

TITLE OF INVESTION: WITH HUMAN DISBASE, METHODS OF BETETION AND USES THEREOF

TITLE RETERRACE, CALOLIO7
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Best Local Similarity 92.5%;
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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PRIOR FILING DATE: 2000-10-03
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                                                                        121 CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT------
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                                           CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGAAGAAGCC
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Pred. No. 1.9e-149
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ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGG--GGCTGGAAGATGGCAGCCCCCGG AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA 482

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CURBENT PILLING DATH: 2000-01-41
FRIOR PAPLICATION NUMBER: 60/241,755
PRIOR PILLING DATE: 2000-0-201,766
PRIOR PILLING DATE: 2000-0-201
PRIOR PILLING DATE: 2000-0-301
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PRIOR PILLING DATE: 2000-0-301
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2782
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Patent No. 6812339
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                        ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG 609
                                                                         AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGG-
                                                                                                                                                                                                                                                                            AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                              CTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGGCCCGTGCAGTTCCTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAGAGTCTATTCCGACACCCTCCAACAGGAGGAAACACAACAGAAATCCAACCTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAACCTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGAAGAAGCC 242
ACMITCCIGCGCATGCTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG 714
                                                                                                                                                          ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC
                                                                                                                                                                                              ACTEGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC
                                                                                                                                                                                                                                                                                                                    AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA
                                                                                                                                                                                                                                                                                                                                                         AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 536.8; DB 4;
Pred. No. 1.9e-149;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----AACCCCCAGACCTCCCTCTGTTTC
                                                                                                                                                                                                                                       - GGCTGGAAGATGGCAGCCCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 821
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483

AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGG-

423

363 256 303 243

436 ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC

376 MAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG

-GGCTGGAAGATGGCAGCCCCCGG

316 AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA

-- MACCCCCAGACCTCCCTCTGTTTC

AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA CTGCTCCGCATCTCCTCGTCATCCAGTCGTCGCTGGAAGCCCGTGCAGTTCCTCAGG CTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAACAACCTAGAG TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACAGAAAATCCAACCTAGAG

48

661

556 ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG 609

ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG

714

ACTGGGCAGATCTTCAAGCAGCCCTACACGAAGTTCGACACAAACTCACACAACGATGAC

660 555 600 49 540 43 379 42 319 36: 255 30 19 242

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US-09-949-016-2783
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Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2783
LENGTH: 821
                                                                                                                                                                                                                                                                                Matches 605; Conservative
                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                   Query Match 88.1%;
Best Local Similarity 92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POINTORNELSWE IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THERBOF
FILE REFERENCE: CLOG1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                          61
                                                                                                                                                                                     63
                                                                                                                                                                                                                                CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGAAGAAGCC
                                               CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT------
                                                                                          CITCAAGAGGGCAGIGCCTTCCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTATG
                                                                                                                                          CTTCAMGAGGGCAGTGCCTTCCCAACCATTCCCCTTATCCAGGCTTTTTGACAACGCTAGT
                                                                                                                                                                                     Score 536.8; DB 4;
Pred. No. 1.9e-149;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                    821
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US-08-187-756C-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: January 27, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 0 ...
STREET: 0 ...
CITY: ROSELAND
CTATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: FERRARO, GREGORY D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN
ADDRESSEE: CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                          181
                                             301
                                                                                      229
                                                                                                                            241
                                                                                                                                                             172 --- TCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAAACGCAGCAG 228
                                                                                                                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGGCTACAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTTGGCCTGCTCTGCCTGGCCTGG 60
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GTGCAGCTCCTCAGGAGCGTCTTCGCCAACAGCCTGGTGTATGGCGCCTCGGAGAGCAAC 348
                                                                              CTCCGCGCCCGTCGCCTGTACCAGCTGGCATATGACACCTATCAGGAGTTT------ 171
                                                                                                                                                                                                                                                                                                                          CITCANGAGGGCAGTGCCTTCCCANCCATTCCCTTATCCAGGCTTTTTGACAACGCTATG 120
                                                                                                                                                                                                                                                                                                                                                                   CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT 120
                                                                                                                                                                                                                                                                                                                                                                                                        ATGGCTGCAGGCTCCCGGACGTCCCTGTCTCTGGCTTTTGGCTCGCCTGTCCCTGG 60
                                     GTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAAC 360
                                                                                                                   AMATICCAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCC 300
                                                                                                                                                                                                                                                                                     CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTAACCCCCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/081877560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             597 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROSEN, ET AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201-994-1700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 503, DB 1,
Pred. No. 1.8e-139;
Nismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                              288
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US-08-710-324A-2
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                                        Matches 552,
                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5962411
                                                                                                                                                                                                                                                            TELEFAX: 301-309-843:
INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen, et al.
TITLE OF INVENTION: Huma
                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                            Local Similarity
                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/187,756
FILING DATE: 27-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          349 GTCTATCGCCACCTGAAGGACCTAGAGGAAGGCATCCAAAGCCTGATGTGGAGGCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 GATUGCAGCCCCCGGACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 GTCTATGACCTCCTAAAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGGAGGCTGGAA 420
3
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                                                                                                                                                                                                                    597 base pairs
                                                                                                                                                                                                                                                                                301-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                            Conservative
                                                                                                                                                                                                                                                                                                    301-309-8504
                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Growth Factor
                                                            90.6%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/710,324A
                                                                                                                                                                                                                                                                                                                                        PETOADI.SKE
                                                        Score 503; DB 2;
Pred. No. 1.8e-139;
                                    Mismatches
                                        45; Indels 12;
                                                                            Length 597;
                                        Gaps
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61 CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT 120

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US-09-411-657-2

, Sequence 2, Application US/09411657

, Patent No. 6566328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                               COMPUTER DEADMALE FORM,
MEDILIN TYPE: PLOPPY disk
COMPUTER: IAM PCORPALIBLE
COMPUTER: IAM PCORPALIBLE
COMPUTER: IEM PCORPALIBLE
COMPUTER: PECCELIN RELEASE BL.O, Version #1.30
CURBENT APPLICUTION DATH:
APPLICATION WOMER: US/09/411.657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rosen, et al.
TITLE OF INVENTION: Human Growth Factor
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE, POCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHCNE: 301-309-8504
                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                            STREET: >--
                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                         FILING DATE:
                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                    PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       589
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US-09-411-657-2
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SEQUENCE CHARACTERISTICS:
SEQUENCE HARACTERISTICS:
LENGTH: 597 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 82.6%;
Local Similarity 90.6%;
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GTCTATGACCTCCTAAAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAAGGCTGGAA
                                      GTGCAGCTCCTCAGGAGCGTCTTCGCCAACAGCCTGGTGTATGGCGCCTCGGAGAGCAAC
                                                                     GTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAAC
                                                                                                       ANATCCANCCINGNGCIGCICCGCNICTCCCTGCTCCATCCAGTCGTGGCTGGAGCCC
                                                                                                                                                                      ---TCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAAACGCAGCAG
                                                                                                                                                                                                        ACCTCCCTCTGTTTCTCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACACAACAG
                                                                                                                                                                                                                                       CTCCGCGCCCGTCGCCTGTACCAGCTGGCATATGACACCTATCAGGAGTTT
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; Pred. No. 1.8e-
0; Mismatches
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US-08-117-809A-1 RESULT 12 Sequence 1, Application US/08117809A Patent No. 5496713 GENERAL INFORMATION: APPLICANT: HONJO, Masaru APPLICANT: YOSHINO, Setsuo

ğ S В

> 469 481 409

541 ATGGACAAGGTCGAGACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGT

ATGGACAAGGTCGAGACATTCCTGCGCATCGTGCAGTGCCGCTCTGTCGAGGGCAGCTGT GATGGCAGCCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAA GTCTATCGCCACCTGAAGGACCTAGAGGAAGGCATCCAAAGCCTGATGTGGAGGCTGGAA

588 600 528 540 468 480 408

421 GATGGCAGCCCCCGGACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAAC

349

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: TITLE OF INVENTION: PROCESS APPLICANT: NAKAYAMA, Akira APPLICANT: NAITO, Naokazu ADDRESSEE: PROCESS FOR PRODUCTION OF HUMAN GROWTH

Burns, Doane,

Swecker & Mathie

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JS-08-117-809A-1
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                             Matches 512;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 859 base pairs
TYPB: nucleic acid
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TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                   PRATURE
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NAME: Crane-Feury, Sharon E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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APPLICATION NUMBER: JP 240936/1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 009911/1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/117,809A
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256 CIGCICCGCATCICCCIGCICCATCCAGTCGIGGCIGGAGCCCGIGCAGTTCCTCAGG 315
                                                                                                    329 GCCTTCCCAACTATACCACTTTCGCGCCTATTCGATAACGCAAGTCTACGTGCTCACCGA 388
                                                                                                                                                                                                    76 GCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGTCTCCGCGCCCATCGT 135
                                  TCAGAGTCTATTCCGACACCCTCCAACAGGGGGGGGAACACAGAAATCCGAACCTAGAG 508
                                                                 TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAACCTAGAG 255
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251..859
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332..859
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251..331
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179..208
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                                                                                                                                                                                                                                       Score 500.6; DB 1; Length 859;
Pred. No. 1.1e-138;
0; Mismatches 19; Indels 0
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809 ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC 859
                                              556 ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC 606
                                                                                                              689 ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC
                                                                                                                                                                                                                                                                                436 ACTOGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC 495
                                                                                                                                                                                                                                                                                                                                                629 AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCÄGCCCCCGG
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US-08-117-809A-2 Patent No. 5496713 GENERAL INFORMATION: Sequence 2, Application_US/08117809# Patent No. 5496713 TITLE OF INVENTION: PROCESS FOR PRODUCTION OF HUMAN GROWTH TITLE OF INVENTION: HORNONE NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: APPLICANT: APPLICANT: APPLICANT: HONJO, Masaru YOSHINO, Setsuo NAKAYAMA, Akira NAITO, Naokazu

ZIP: 22313-1404 COMPUTER READABLE FORM: COUNTRY: United States STREET: George M CITY: Alexandria ADDRESSEE: Burns, Doane, Swecker & Mathis Virginia George Mason Bldg., Washington & Prince Sts

CURRENT APPLICATION DATA: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS FILING DATE: APPLICATION NUMBER: SUPTWARE: Patentin Release #1.0, Version #1.25 09-SEP-1993 US/08/117,809J

PRIOR APPLICATION DATA:

APPLICATION NUMBER: CLASSIFICATION:

JP 240936/1992

ATTORNEY/AGENT INFORMATION: PRIOR APPLICATION DATA: FILING DATE: APPLICATION NUMBER: 25-JAN-199: JP 009911/1993

TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO: NAME: Crane-Feury, Sharon E REGISTRATION NUMBER: 36,113 REFERENCE/DOCKET NUMBER: 02 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620 36,113 029430-163

TOPOLOGY: linear MOLECULE TYPE: DNA ORIGINAL SOURCE: SEQUENCE CHARACTERISTICS STRANDEDNESS: LENGIH: nucleic acid DNA (genomic) double

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US-08-187-756C-1
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                                                                                                          Sequence 1, Application US/08187756C
Patent No. 5597709
                                                GENERAL INFORMATION:
APPLICANT: ROSEN, ET AL.
TITLE OF INVENTION: Huma
NUMBER OF SEQUENCES: 7
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                                CORRESPONDENCE ADDRESS:
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FEATURE:
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OTHER INFORMATION:
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                                                                                                                                                                                                ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC 859
                                                                                                                                                                                                                       ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC 606
                                                                                                                                                                                                                                                             ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIGCICCGCATCICCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAGAGTCTATTCCGACACCCCTCCAACAGGGAAGAACACAACAGAAATCCAACCTAGAG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIGCACCAGCIGGCCTTTGACACCTACCAGGAGTTTAACCCCCAGACCICCCCTCTGTTTC 195
                                                                                                                                                                                                                                                                                                                                                                                        AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG
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CARELLA, BYRNE, BAIN, GILFILLAN,
CECCHI, STEWART & OLSTEIN
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332..859
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251..331
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251..859
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promoter."
                                                             Growth Hormone
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Pred. No. 9.8e-138;
0; Mismatches 21;
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CITCAMGAGGGCAGIGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTATG 120 CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTTGACAACGCTAGT 120

436 376 361 316 301

ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC ACTOGGCAGATOTTCAATCAGTCCTACAGCAAGTTTGACACAAAATCGCACAACGATGAC ANGGACCTAGACGANGGCATCCAAACGCTGATGTGGAGGCTGGAAGATGGCAGCCCCCGG ANGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG AGCGTCTTCGCCAACAGCCTGGTGTATGGCGCCTCGGAGAGCAACGTCTATCGCCACCTG AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA CTGCTCCGCATCTCCCTGCTGCTCACTCAGTCATGGCTGGAGCCCGTGCAGCTCCTCAGG TCAGAGTCTATTCCAACACCTTCCAACAGGTGAAAAACGCAGCAGAAATCTAACCTAGAG

540 495 480 435 420 360 315 300 255 240

256 CTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGAGCCCGTGCAGTCCTCAGG

196 TCAGAGTCTATTCCGACACCCCTCCAACAGGGAAGGAAAACACAGAAAATCCAACCTAGAG 181 TATATOCTGAAGGAGCAGAAGTATTCATTCCTGCAGAACCCCAGACCTCCCCTCTGCTTC 121 CTCCGCCCCTTCGCCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGAAGAAGCC 180 121 CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCCTACCAGGAGTTT-----

AACCCCCAGACCTCCCTCTGTTTC

171

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US-08-187-756C-1
                                                                        Matches
                                                                 Query Match 81.0%;
Best Local Similarity 87.3%;
Matches 571; Conservative
                                                                                                  Query Match
                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                TOPOLOGY: LI
MOLECULE TYPE:
                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/187,756C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                 TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-55
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: January 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                   ATGGCTACAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCCTGCCCTGG 60
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ATGGCTGCAGGCTCCCGGACGTCCCTGCTTGGCTTTTTGGCCTGCTCTGCCTGTCCTGG
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NEW JERSEY
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                                                              Score 493.2; DB 1;
Pred. No. 1.5e-136;
0; Mismatches 38;
                                                                 Indels 45;
                                                                                              Length 654;
                                                              Gaps
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RESULT 15
US-08-710-324A-1
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Patent No. 5962411
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brookes, A. Anders
REGISTRATION NUMBER: 56,773
RETERENCE/DOCKET NUMBER: PF104D1.SKB
TELECOMMUNICATION IMPORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/187,756
FILING DATE: 27-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: mucleic acid
STRANDEDNESS: gingle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
FILING DATE: 16-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Human Genome Sciences, Inc
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196 TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAACCTAGAG 255
                                           172
                                                                                                                                                                                  121 CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT------ 171
                                                                                                                                                                                                                                       61 CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTATG 120
                                                                                                                                                                                                                                                                              61 CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT 120
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                                                                                                                                           CTCCGCGCCCGTCGCCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGAAGAMGCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                              81.0%; Score 493.2; DB 2; Length 654;
87.3%; Pred. No. 1.5e-136;
ative 0; Mismatches 38; Indels 45
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                                                                                                ----AACCCCCAGACCTCCCTCTGTTTC 195
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                                                                                                                                                                                                                                                                                                                                                                                                                     316 AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 CTGCTCCGCATCTCCCTGCTGACTCACTCATGGCTGGAGCCCGTGCAGCTCCTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 CINCTECGEATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                556 ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGCAGCTGTGGCTTCTAG 609
                                                                                          436 ACTROGGCAGATCTTCNAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC 495
ACATTCCTGCGCATCGTGCAGTGCGGCTCTGTGGAGGGCAGCTGTGGCTTCTAG 654
                                                                                                                                          ACTEGECAGATOTTCANTCAGTCCTACAGCANGTTTGACACAAAATCGCACAACGATGAC 540
                                                                                                                                                                                                                                                                                    AAGGACCTAGACGAAGGCATCCAAACGCTGATGTGGAGGCTGGAAGATGGCAGCCCCCGG
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Search completed: February 7, 2005, 12:30:44 Job time: 166 secs

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nucleic search, using
                                     Copyright (c) 1993 - 2005 Compugen
8W
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Sequence: OM nucleic -91 score: February 7, 2005, 11:40:04, Search time 477 Seconds (without alignmente) 348:526 Willion cell updates/sec US-09-856-796B-1 atggctacaggctcccggac.....agggcagctgtggcttctag 609

Scoring table: Gapop 10.0 , Gapext 1.0 4313806 seqs, 2877871033 residues

> 472 473 473 472 472

US-10-621-693-54 US-09-876-478-1

US-10-621-693-73 US-10-621-693-46 US-10-621-693-7 US-09-819-094-19 US-09-373-967-3 US-10-821-273+73

US-10-477-651-1 US-10-289-845-1 US-10-287-994-47 US-10-410-913-47 US-10-411-012-47 US-10-410-997-4"

> sequence Sequence

US-10-621-693-85 US-10-621-693-67 US-10-621-693-75 US-10-621-693-81

Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli Sequence 65, Appl Sequence 65, Appl Sequence 10, Appl Sequence 10, Appl Sequence 17, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB Post-processing: seq length: 0 length: 2000000000

Minimum Match 0% Maximum Match 100% Listing first 45 sr Summaries

Comment (Appendix and Appendix and Appendix and Appendix

No. is the number of results predicted by chance to hap are a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

SUMMARIES

Regult õ Score Match Length

554 US-09-853-688-1 US-09-853-688-3 Description

US-10-788-318-1 8 US-10-788-318-3 0 US-09-969-748C-3 0 US-09-969-178C-3 - US-09-804-409A-17 7 US-10-411-037-47 7 US-10-411-026-47 7 US-10-411-962-47 Sequence 1, Appli Sequence 3, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 47, Appl Sequence 47, Appl Sequence 47, Appl Sequence 47, Appl Sequence 47, Appl

549.2 549.2 549.2 550.8

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4470.88 4470.88 4470.88

472 . US-10-621-693-44 US-10-621-693-7 US-10-621-693-52 US-10-621-693-65 US-10-621-693 US-10-621-693-50 US-10-621-693-US-09-984-010 US-10-621-693-79

US-10-621-693-83

sequence 73, Appl sequence 79, Appl sequence 79, Appl sequence 72, Appl sequence 41, Appl sequence 41, Appl sequence 40, Appl sequence 50, Appl sequence 52, Appl sequence 67, Appl sequence 15, Appl sequence 15, Appl sequence 15, Appl sequence 15, Appl sequence 15, Appl sequence 15, Appl sequence 16, Appl sequence 17, Appl sequence 17, Appl

ALIGNMENTS

US-09-853-688-1

Sequence I. Application Us/9895688
Facan No. US@000001656A1
GENERAL INFORMATION: NUT
NOTICE OF THE SEQUENCE OF

NUMBER OF SEQ ID NOS: 66 SOFTWARE: PatentIn Ver. 2 SEQ ID NO 1 LENGIH: 654 FILE REFERENCE: WCM78
CURRENT APPLICATION NUMBER: US/09/853,688
CURRENT FILING DATE: 2001-05-14

US-09-853-688-1 ORGANISM: Homo FEATURE: NAME/KEY: CDS TYPE: DNA sapiens

Query Match Local Similarity 91.0%, Score 554; DB 9; 1 Pred. No. 2.6e-164; 0; Mismatches 0; Length 654

Matches 609; 61 CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT ATGGCTACAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTTGGCCTGCTCTGCCCTGC Conservative Indels 45, Gaps 120 60 60

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US-09-853-688-3
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NATICANT: GEROOM: ANNE M
NATICANT: GEROOM: ANNE
TITLE OF INVESTION DATES
TITLE OF INVESTION: HANNE: THE VERAFICOS AND THEIR URSS
TITLE REFERENCE: ANYTHOUSE HANNE: THE VERAFICOS AND THEIR URSS
TITLE REFERENCE: ANYTHOUSE HANNE: THE VERAFICOS AND THEIR URSS
TITLE REFERENCE: ANYTHOUSE ANY DATES OF THE VERAFICOS AND THEIR URSS
CHEMICAL TO STREET AND ANY THE ANY THE VERAFICOS AND THEIR URSS
UNDERSTREET FILMED DATES. AND A CO. 1-5-14
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Patent No. US20020081605A1
                                                                                            Matches 609;
                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                     LOCATION: (1) .. (651)
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                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                        ENGTH: 654
                                                                                                                   Local Similarity
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ATGGCTACAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCCTGG 60
                           ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG
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                                                                                            Conservative -
                                                                                                              93.14;
                                                                                       0
                                                                                                              Score 554; DB 9; Length 654;
Pred. No. 2.6e-164;
                                                                                       Mismatches
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Publication No. US20040137510A1.
GENERAL INFORMATION:
Query Match 91.0%;
Best Local Similarity 93.1%;
Matches 609; Conservative
                                                                                                                                                                                                                       SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 654
                                                                                                                                                                                                                                                                                                             FILE REFERENCE: WCM78
CURRENT APPLICATION NUMBER: US/10/788,318
CURRENT FILING DATE: 2004-03-01
                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS TITLE OF INVENTION: HUMANS, THE VARIATIONS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: PROCTER, ANNIE M.
APPLICANT: GREGORY, JOHN
APPLICANT: MILLAR, DAVID S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: COOPER, DAVID N.
                                                                                                                             PEATURE:
NAME/KEY: CDS
                                                                                                                                                                          ORGANISM: Homo
                                                                                                                                                                                                     TYPE: DNA
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Score 554; DB 18;
Pred. No. 2.6e-164;
0; Mismatches 0;
                                        Length 654;
Indels
45;
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Indels 45;

Matches 609; Conservative Local Similarity 93.1%; Score 554; DB 18; Length 654 Pred. No. 2.6e-164; 0; Mismatches 0; Indels

FEATURE: NAME/KEY: CDS ORGANISM: Homo sapiens TYPE: DNA

SEQ ID NO 3 LENGTH: 654

SUFTWARE: PatentIn Ver. 2.1

APPLICANT: PROCTER, ANNIE M.
APPLICANT: GREGORY, JOHN APPLICANT: COOPER, DAVID N.

Sequence 3, Application US/10788318
Publication No. US20040137510A1
GENERAL INFORMATION:

APPLICANT: MILLAR, DAVID S.
TITLE OF INVENTION: HEPODE FOR DETECTING GROWTH HORMONE VARIATIONS
TITLE OF INVENTION: HUMANS, THE VARIATIONS AND THEIR USES

H

-10-788-318-3 FILE REFERENCE: WCM78
CURRENT APPLICATION NUMBER: US/10/788,318
CURRENT FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 66 LOCATION: (1)..(651)

US-10-788-318-3

601 556 541 496 481 436 421 376 361 316 301 256 241 181 172 121 61

ACATTICTISCOCATCGTGCAGTGCAGTGTGTGAGGGCAGCTGTGGCTTCTAG 609 GCACTACTCAMGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCGAG 600

556 601 541 496

ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG 654 ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG

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> ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGCTTCGACACAAACTCACACAACGATGAC ACTOGGCAGATCTTCANGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC 540 495

AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG 480

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301 CTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCCGTGCAGTTCCTCAGG 256 CTGCTCCGCATCTCCTGCTGCTCATCCAGTCGTGGAGCCCCGTGCAGTTCCTCAGG AGIGTCTTCGCCAACAGCCTGGIGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA

375

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375 360 300 240 198 180

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61 CITCAAGAGGGCAGIGCCITCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT 120 60

Page 3

US-09-969-748C-3 / Sequence 3, Application US/09969748C / Publication No. US20030161809A1 GENERAL INFORMATION: APPLICANT: APPLICANT: ARIZEKE PHARMACEUTICALS,

HOUSTON, LOU, L.
SHERIDAN, Philip, J.
HAWLEY, Stephen
GLYNN, Jacqueline, M.
CHAPIN, Steven
BASU, Amaresh

APPLICANT: APPLICANT: APPLICANT:

TITLE OF INVENTION COMPOSITIONS AND METHODS FOR THE TRANSFORT OF BIOLOGICALLY ACTIVE TITLE OF INVENTION AGENT ACCESS CELLULAR BARRIERS
FULL REFERENCE, 057326-010
CURBENT APPLICATION METHERS. 10,500-74-0.
CURBENT FILLING DATES. 2002-72-19
CURBENT FILLING DATES. 2002-72-19
COURSETT FILLING DATES. 2002-72-19
COURSETT FILLING DATES. 2002-72-19
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COURSETT FILLING DATES. 2002-72-19
COURSETT FILLING DATES. 2002-72-19
COURSETT FILLING DATES.

PRIOR APPLICATION MUMBER: US 60/267,601
PRIOR PRIOR PRICE 2001-20,90
PRIOR APPLICATION MUMBER: US 60/248,819
PRIOR APPLICATION MUMBER: US 60/248,478
PRIOR APPLICATION MUMBER: US 60/248,478
PRIOR APPLICATION MUMBER: US 60/237,929

Indels 45 Gaps

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                                                              US-09-804-409A-17
                                                                                                                                                      FILE REFERENCE: 02996/027 9721
CURRENT APPLICATION HYMERE US/09/804,409A
CURRENT PFILMS DATE: 2001-03-12
NUMBER OF SED ID NOS: 19
SED ID NO 17
LENGTH: 799
LENGTH: 799
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APPLICANT: AUTHORY AUTHORY T.
APPLICANT: GENERA, CHAPGHOY TO.
APPLICANT: GENERA, CHAPGHOY TO.
APPLICANT: GENERAL CHAPGHOY TO.
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Patent No. US20020155100Al
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      Score 549.2;
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Publication No. US20040043446A1
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APPLICATI, CHAM, MANACHCHIDASE A. BEMORELIMO AND GLYCOCOMUTENTION OF ALPHA

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APPLICATION CHAMPACH SEE J. (8 / 13/8-523)
                                                                                                    PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
            PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
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Zopf, David
Bayer, Robert
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PRIOR FILING DATE: 2002-07-17
PRIOR PRIDE FLING DATE: 2002-08-18
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SEQTPAGE: PRICE TIME OF SEQ ID NOS: 75
                                                                                               Sequence 47, Application US/10411026
Publication No. US20040063911A1
GENERAL INFORMATION:
                   APPLICANT:
APPLICANT:
APPLICANT:
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LENGTH: 799
                                                                       APPLICANT: Neose Technologies,
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ORGANISM: Homo
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Pred. No. 9.1e-163;
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GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAAGGACATGGACAAGGTCGAG ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTTGGAAGATGGCAGCCCCCGG

640 580 495 520 435 460 400 315 340 255 195

ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA CTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG CTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG

376

341 256 281

316 AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA 375

556 ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG

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PRIOR APPLICATION NUMBER: US 60/991,777
PRIOR FILMEN DATE: 2002-06-12
PRIOR FILMEN DATE: NUMBER: US 60/369,594
PRIOR FILMEN DATE: NUMBER: US 60/369,594
PRIOR FILMEN DATE: 2002-06-16
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LENGTH: 799
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Best Local Similarity
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PRIOR FILLING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILLING DATE: 2002-06-07
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CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
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APPLICANT: Chem, Xi
TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED
TITLE OF INVENTION: METHODS
TILE REFERENCE: 040833-01-063
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ORGANISM: Homo
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CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGAAGAAGCC
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Pred. No. 9.1e-163;
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US-10-410-962-47
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Publication No. US20040077836A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 92. Matches 606; Conservative
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LENGTH: 799
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CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.2
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PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
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PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
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APPLICANT: DeFrees, Shawn
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FILING DATE: 2002-06-25
APPLICATION NUMBER: US 60/396,594
FILING DATE: 2002-07-17
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                                                                                                           CTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG 315
                                                                                                                                                   TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACAGAACAGAAATCCAACCTAGAG
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Chen, Xi
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Bayer, Robert
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Pred. No. 9.1e-163;
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                                                                                                                                                                                                                                                                   Matches 606;
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US-10-411-049-47
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                                                                                                                                                                                                                                                                                                        Sequence 47, Application US/10411049
Publication No. US20040082026A1
CURRENT APPLICATION NUMBER: US/10/411,049
                          TITLE OF INVENTION. INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
TITLE OF INVENTION. ALPHA
FILE REPERENCE: 04085-01-5055
                                                                                                    APPLICANT:
                                                                                                                              APPLICANT:
                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                   APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
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                                                                                               Bowe, Caryn
                                                                                                                                                                                                         DeFrees, Shawn
Zopf, David
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US-10-411-049-47 SEQ ID NO 47 LENGTH: 799 SOFTWARE: Patentin version 3.2 PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249 PRIOR APPLICATION NUMBER: US 60/387,292 PRIOR FILING DATE: 2002-06-07 PRIOR APPLICATION NUMBER: US 60/391,777 PRIOR APPLICATION NUMBER: US 60/328,523 PRIOR FILING DATE: 2001-10-10 PRIOR APPLICATION NUMBER: US 60/344,692 CURRENT FILING DATE: 2003-04-09 NUMBER OF SEQ ID NOS: 75 PRIOR APPLICATION NUMBER: US 60/407,527 PRIOR FILING DATE: 2002-08-28 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2001-10-19 ORGANISM: Homo TYPE: DNA sapiens

121

CTCCGCGCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT-----

61 CTTCAAGAGGGCAGTGCCTTCCCCAACCATTCCCCTTATCCAGGCTTTTTTGACAACGCTAGT 120

Conservative

0; Mismatches Pred. No. 9.1e-163;

Indels 45; Length 799;

Gaps 60

90.24;

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-410-930-47
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Publication No. US20040115168A1
                                                                                              SEQ ID NO 47
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                                                                                                                                           PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/410,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 040853-01-5056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
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                                                                          LENGTH: 799
                                                                                                                                                                                                                                                                   RAPPLICATION NUMBER: US 60/391,777
FILING DATE: 2002-06-25
APPLICATION NUMBER: US 60/396,594
FILING DATE: 2002-07-17
                                                                                                                                                                                                                                                                                                                                                             PILING DATE: 2001-10-19
APPLICATION NUMBER: US 60/387,292
PILING DATE: 2002-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/344,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-10-10
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Bowe, Caryn
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Hakes, David
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Matches 606; Conserv
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                                                                                                                   376 AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG
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ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG 694
                                                                              ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC
                                                                                                                                                                                                                                           ANGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG
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pred. No. 9:1e-163;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -AACCCCCAGACCTCCCTCTGTTTC 195
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US-10-411-012-47
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                                                                               Sequence 47, Application US/10411012
Publication No. US20040132640A1
GENERAL INFORMATION:
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LENGTH: 799
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Best Local Similarity 92.7%;
                       APPLICANT:
                                                   APPLICANT: Neose Technologies, 'Inc.
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PRIOR APPLICATION INUBER: US 60/396,594
PRIOR PILING DATE: 2002-07-17
PRIOR APPLICATION UNMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
   APPLICANT
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SOFTWARE: PatentIn version 3.2
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PRIOR FILING DATE: 2002-08-28
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ORGANISM: Homo sapiens
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Zopf, David
Bayer, Robert
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Pred. No. 9.1e-163;
0; Mismatches 3;
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; TYPE: DNA
; ORGANISM: Homo
US-10-411-012-47
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 47
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ANGGACCTAGAGGANGGCATCCANACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG
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90.2%;
Best Local Similarity 92.7%;
Matches 606; Conservative
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PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
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PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
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PRIOR FILING DATE: 2002-08-28
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PRIOR FILING DATE: 2002-08-16
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PRIOR FILING DATE: 2002-07-17
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PRIOR FILING DATE: 2002-06-25
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Score 549.2; DB 18
Pred. No. 9.1e-163;
0; Mismatches 3;
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Best Local Similarity 92.7%;
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LENGTH: 799
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Publication No.
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SOFTWARE: PatentIn version 3.1
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PRIOR FILING DATE: 2002-08-28
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PRIOR FILING DATE: 2002-06-07
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PRIOR FILING DATE: 2001-10-19
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CURRENT FILING DATE: 2002-11-05
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ORGANISM: Homo sapiens
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** FILING DATE: 2002-07-17
** APPLICATION NUMBER: US 60/404,249
**FILING DATE: 2002-08-16
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FILING DATE: 2002-06-25
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Bowe, Caryn
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Pred. No. 9.1e-163;
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No. US20040142856A1
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GENERAL INFORMATION:
FILE REFERENCE: 040853-01-5081
CURRENT APPLICATION NUMBER: US/10/410,913
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
                                                                                                                                                         TITLE OF INVENTION: GLYCOCONJUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Neose Technologies,
APPLICANT: DeFrees, Shawn
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                                                                                                                                                                                                       Chen, Xi
Bowe, Caryn
                                                                                                                                                                                                                                                                                                    Zopf, David
                                                                                                                                                                                                                                                           David
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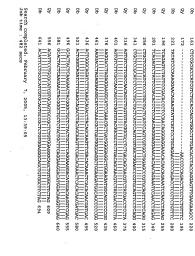
SEQ ID NO 47 SOFTWARE: PatentIn version 3.2 NUMBER OF SEQ ID NOS: 75 PRIOR FILING DATE: 2002-08-28 PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2002-08-16 PRIOR APPLICATION NUMBER: US 60/396,594 PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25 PRIOR APPLICATION NUMBER: US 60/387,292 PRIOR FILING DATE: 2001-10-19 LENGTH: 799 APPLICATION NUMBER: US 60/407,527 US 60/404, 249

US-10-410-913-47 Query Match Best Local Similarity Matches 606; Conservative 90.2%; Score 549.2; DB 18 Pred. No. 9.1e-163; Mismatches DB 18; Indels 45; Length Gaps

ORGANISM: TYPE: DNA

Homo

å 100 60



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278.5			374.5			421.5	449	465	467.5	471.5	480	536	542	550	551	596	598	601	602	603	643.5	199	666	666	666	672	677	679	682	682
25.0	25.1	25.1	33.7	34.8	35.5	37.9		41.8		42.4	43.2	48.2	48.7	49.5	49.6	53.6	53.8	54.0	54.1	54.2	57.9	59.4	59.9	59.9	59.9	60.4	60.9	61.1	61.3	61.3
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AlCoses-réderances UNIPADI(PAIA); del VOSSAO A)NOSE: the 20% Anotr form searcorpoin lactor seridues 58-72 (32-46 in the active hormon Rochem, EX.7; islaw, Y.C.; shith, D.H.; Barrear-Saldana, H.A.; Gelinam, R.E.; Seeburg, P. Genomics 4, 479-497, 1989 A)Title: The human growth hormone leueur mucleotide sequence, biology, and evolution. A)Sederescoe number; A24325; WIDID#S907977; MRID:774450 A;Accession: A32435

A; Molecule type: DNA A; Residues: 1-217 < CHE>

A/Cross-references (Baj0)071; NID;g181149; FIDN:ANA5549.1; FID:g181149
A/Robaim, M.; Rosgon, R.
A/Robaim, M.; Rosgon, R.
A/Robaim, M.; Rosgon, R.
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A/Robaim, M.; Rossel, MID:Rosselde sequence of the human growth hormone structure
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A/Robaimsence number (MID:Rosselde sequence of the human growth hormone structure) A;Accession: A93694

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A;Molecule type: protein *
A;Residues: 27-34, L', 36-47 <ROB>
R;de Vos, A.M.; Ultsch, M.; Kossiakoff,
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Bloches, Biophys, Res. Commun. 2, 511-516, 1980

Riches, Biophys, Res. Commun. 2, 511-516, 1980

Ariticle: The 20,000-dailon variant of hemm growth bormone: location of the Anitic
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A;Accession: S09685
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R;Robson, V.M.J.; Ree, I.D.; NG, P.
Biol. Chem. Hoppe-Seyler 371, 423-441, 1990
A;Title: Identification of the aspartimide structure in
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A; Residues: 27-57;73-79 < CHA>
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A; Residues: 27-217 <BEW>
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RiBedley, T.A.; Dixon, J.S.; Li, C.H.
RiBedley, T.A.; Dixon, J.S.; Li, C.H.
A.Title: Segunce comparison of human pituitary growth hormone,
A.Toterence number: A91764; MUID:73092028; PMID:4675454
A.Roference number: A91764; MUID:73092028; PMID:4675454
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A;Residues: 119-120;157-159 <NI2>
R;Niall, H.D.
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A.Teference number: A93397; MUID:71139765; PMID:5279046
A;Accession: A93397
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Arch. Blochem. Blooplys. 146, 233-235, 1971
AvTitle: Human pituitary growth hormone. XXXII. The primary structure of the
AvReference number: A90051; MUID:72143935; PMID:5144027
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Protein Chem. 2, 425-436, 1983
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A.Title: Sequences of Dituitary and placental lactogenic and growth Reference number: A3978; MID:7115396; MID:5279528
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A; Residues: 27-51 < NIA>
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;Residues: 27-69 <SIN>
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A;Gene: GDB:GH1
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A; Residues: 1-26 < RES>
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Science 255, 306-312, 1993
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A, Title: Periplasmic production of correctly processed A, Reference number: I41126, MUID:86137333, PMID:3912261 A, Accession: I84549 human growth hormone in Escherich

Status: preliminary; translated from GB/EMBL/DDBC

A;Cross-references: GB:M14398; NID:g183158; FIDN:ANA5554.1; FID:g183159 G;Comment: The gene for this hormone is transcribed only in somatotrophic G;Comment: About 90 of somatotrophi is the 22K long form. Bomatotrophic cells of

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widep position: 17921-179213
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US-09-856-796B-1 (1-609) x STHU (1-217) MetAlaThrGlySerArgThrSerLeuLeuLeuAlaPheGlyLeuLeuCysLeuProTrp

LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPheGluGluAla CICCGCGCCCATCGICIGCACCAGCIGGCCTTTGACACCTACCAGGAGITIT-----

40 20

TyrIleProLysGluGlnLysTyrSerPheLeuGlnAsnProGlnThrSerLeuCysPhe -AACCCCCAGACCTCCCTCTGTTTC 60 80

SerGluSerIleProThrPro TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAAACACAGAAAATCCAACCTAGAG SerAmArgGluGluThrGlnGlnLysSerAmLeuGlu 100 255

CTGCTCCGCATCTCCCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG 315

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Chacessica: 15/1112, JAS98 Hengemenc_gevision 11-May-1996
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Chacessica: 15/112, JAS98 Hengemenc_gevision to the Change
Aprilla: Claiming of Cour growth hormone/horionic momentamentropin-related complementament (51)
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A;Reference number: A44774
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A;Molecule type: protein
A;Mole: the monkey species is not identified in
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Arch. Biochem. Biophys. 245, 287-291, 1986
A.Title: The primary structure of monkey pituitary growth
A.Reference number: A05094; MUID:86129460; PMID:3080959
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A; Residues: 1-217 < RES>
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A; Residues: 1-217 < CHE>
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LysaspieuGluGlyIleGinThrLeuMetGlyArgLeuGluAspGlySerSerArg
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ThrPheLeuArgIlevalGlnCysArgSerValGluGlySerCysGlyPhe 217
                                                    ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC 606
                                                                                                              AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysIleGlu
                                                                                                                                                                  ThrGlyGlnIlePheLysGlnThrTyrSerLysPheAspThrAsnSerHisAsnAsnAsnAsp
                                                                                                                                                                                                                                                                                 ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACGATGAC
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N;Alternate names: growth hormone 2; growth hormone variant; hGH-V; placental somatotrop. N;Onteins: somatotropin 2, long splice form; somatotropin 2, short splice form

Cignocia: Mono sepione (anni)
Cignocia: 17-bec; 198 (sequeno; evision; 1.5 eb.)-1958 (text_change 09-Jul-2004
Cibles 17-bec; 198 (sequeno; evision; 1.0 to 4.5 eb.)
Cibles 8.V.; Liko, Y.C.; Sakth, D.H.; Barrere-Saldana, H.A.; Galinas, R.E.
Ganoalies 4, 499-497, 1989
An'Itle: Tib huana growth bormon locus; muclescide sequence, biology, and
Alekierence maher; 1.34353 (MIDS907277); MRIJ-2744780 biology, and evolution Gelinas, R.E.;

ACCess references: UNIFORT POIZ42: GB.30071; MID.9181148; FIDR:AAA52552.1; FID.9181152; RC.0068, M.S.; PRW, J., BERCY, GG.7; Liabhbhort, S.A.
7. Bloi. Comm. 263; 9001-9006; 1988
A.Filler: Two distincts genetise of human growth hormone-variant mRNA in the human placente A.Filler: Two distincts genetise of human growth hormone-variant mRNA in the human placente A.Filler: Two distincts genetise of human growth hormone-variant mRNA in the human placente A.Filler: Two distincts genetise genetises are described to the common genetic genetic genetic and the common genetic ge

A;Title: The human growth hormone gene family: nucleotide sequences show A;Reference number: A01511; MUID:83182010; PMID:7169009 recent diverge

Arbedende (1979: e80Å).
Albedene (1971: 680Å).

the growth hormone-V

A;Note: partial glycosylation was demonstrated by C;Comment: This gene is expressed by the placenta lectin binding

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dhorionammotropin B precurpor - human
NALternate names; horionic smacrommotropin 2
C.Specias; Homo saplams (man)
C.Dates 129-Dec.1398 #Enquence_revision 22-Dec.1399 #rext_change 09-Uni-2004
C.Accession: E2235
R.Chom, E.Y., i.Lov, Y.C.; Smith, D.H.; Barrera-Saldama, H.A.; delinas, R.E.
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                                                                                                                                                                                                                                                                                                                                                                                      AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                ThrGlyGlnIlePheAsnGinSerTyrSerLysPheAspThrLysSerHisAsnAspAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysAspLeuGluGluGlyIleGlnThrLeuMetTrpArgLeuGluAspGlySerProArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG
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88.02%
86.18%
84.49%
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choriomanmotropin A precursor [validated] - human
NyAlternate names: chorionic somatomammotropin 1;
C:Spacies: Homo sapiens (man)
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Barrera-Saldana, H.A.; Gelinas, R.E.;

Seeburg,

somatomammotropin 1, placental lactoger

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Query Match:
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A.7%tils: The human growth hormone locus: nucleotide sequence,
A.Reference number: A32435, MUID:89307277; PMID:2744760
A.Accession: E32435
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Best Local Similarity:
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A; Residues: 1-217 < CHE>
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ThrPheLeuargMetValGlnCysargSerValGluGlySerCysGlyPhe
                                           ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC 606
                                                                              AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu
                                                                                                                              ThrGlyGlnIleLeuLysGlnThrTyrSerLysPheAspThrAsnSerHisAsnHisAsp
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                                                                                                                                                                                                                                                        LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerArgArg
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873.50
84.33*
79.26*
78.55*
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Mismatches:
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A.(Coosa-references: GB.M9543), NID.9506822
RS.Berwood, L.K., Burstein, Y., Schheibter, 1979
Pocc. Natl. Acad. Sci. U.S.A. 76, 1819-1823, 1979
A.Title: Primary Enrocture of the NM2-terminal actra piece of the precursor A.Reference number: 38883, MUD:80034970; MMD:83043
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R.Goodman, H.M., DeNoto, F., Piddes, J.C., Hallweall, R.A.; Page, G.S.; Smith, B.S.; Tisch
Mobilization and Ressembly of Genetic Information, Scott, M.A., Werner, R., Joseph,
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C.Accession: C33455, 594422; 553422, 593931, 593192, 590564, 594947, M.12881
R.Chen, E.Y., Liaso, Y.C., Smith, D.H., Barrers-Saldans, H.A., Gelinss, R.E.,
Genodica, 4, 479-479, 1398
                                                                                                  A;Note: Choriomemoctropin apparently copurified with placental Risherwood, L.M., Handwerger, S., McLaurin, W.D., Lammer, M. Neutre Rew Hiol. 23), 59-61, 1971
A;Title: Aaito-acid sequence of human placental lactogen. A;Reference number: A3401; MUID:72016313; PMID:5286363
                                                                                                                                                                                                                                                                                                                                           Biochem. Soc. Trans. 19, 20S, 1991
A;Title: Catechol-O-methyltransferase from
A;Reference number: A61283; MUID:91244006;
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A; Residues: 27-217 < NIA>
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A, Accession: A94427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in Prolactin and Carcinogenesis, Proc. Fourth Tenovus Workshop Prolactin, Griffiths, A,Title: The chemistry of the human lactogenic hormones.
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A; Residues: 27-217 <LIC>
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A.Title: Amino acid sequence of human chorionic somatomammotropin
A;Reference number: A90054; MUID:73201971; PMID:4712450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Experimental source: placenta
R,Li, C.H.; Dixon, J.S.; Chung, D.
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R:Bhine, J.; Seebusg, P.H.; Martial, J.A.; Baxter, J.D.; Goodman,
Mature 270, 494-499, 1977
Affithe: Construction and analysis of secombinant DNA for human o
A;Reference number; A93192; MID:78071761; PMID:593368
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A; Residues: 1,3-26 <SHE>
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Biochem. Int. 16, 207-292, 1986
A.Title: CHNA cloning of human choronic enomicropin-1 mRNA whose transcription
A.Reference mumber: 15342; MRIO188050958; PMID:885959
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A; Residues: 1-217 <GOO>
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                             Nature New Biol
                                                          R, Sherwood,
                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 27-46 < NIC>
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R; Nic A Bhaird, N.; Tipton, K.F
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A,Residues: 1-3 <TAN>
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: redmun
                       L.M., Handwerger, S.;
Biol. 235, 64, 1972
                                                                                 annotation
                                                          McLaurin,
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PMID:2037148
                                                          W.D.; Lanner,
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Seeburg, P:
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A;Residues: 1-217 <RES>
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A; Residues: 160-217 < RE2>
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;Keywords: hormone; placenta
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AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA
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A; Contents: annotation
R; Schneider, A.B.; Kowalski, K.; Russell, J.; Sherwood,
S: Biol. Chem. 254, 3782-3787, 1979
dimeric human placental
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Article Zemelfosten of the interchain desarteds before of director backcomes on many areas; purposed and areas of the second a Evidence

for CWO lac fu

A;Status: translated from GB/EMBL/DDBJ

Alcome-references: GB:802401; MB:0981109; PIDM:AMA5115.1; PID:0981111 Rseeburg P.H.; Shima, J.; Mertial, J.A.; Ulltich, A.; Goodman, H.121 Frame. Amonc. Am. Physicians 90, 109-116; 1977 [cd. processes of the Apriles: National Amongenee of a Manama gone Goding for a polypspilde hormone Apriles: National Amongenee of a Manama gone Goding for a polypspilde hormone Apacetesians masker: 139589; MID:0815079; PMID:815679
Apacetesians: 139589; MID:08150797; PMID:815679
Apacetesians: 139589; MID:0815079787;

A,Status: translated from GB/EMBL/DDBJ

A;Cross-references: GB:M25118; NID:g181124; PIDN:AAA35721.1; PID:g181125

A; Map position: 17g22-17g24 A; Introns: 4/1; 57/3; 97/3; 152/3 A,Cross-references: GDB:119084; OMIM:150200

pi-Joid/Demain signal empunno éstatus experimental dATOs P327-137/Product: Obordomamoscopin A éstatus experimental dATOs P379-139/JSHAITide bonde: Hentus experimental P379-139/JSHAITide bonde: Interchain (to 215 in dimeric form) éstatus P328/JSHAITide bonde: interchain (to 215 in dimeric form) éstatus P328/JSHAITIde bonde: interchain (to 216 in dimeric form) éstatus P328/JSHAITIde bonde: interchain (to 216 in dimeric form) éstatus

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MetAlaProGlySerArgThrSerLeuLeuLeuAlaPheAlaLeuLeuCysLeuProTrp 20	ATGCTACAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGG 60
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LeuGlnGluAlaGlyAlaValGlnThrValProLeuSerArgLeuPheAspHisAlaMet CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT 40

121 CTCCGCGCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT------

LeuGlnAlaHisArgAlaHisGl nLeuAlaIleAspThrTyrGlnGluPheGluGluThr 60 195

TCAGAGTCTATTCCGACACCCTCCAACAGGAGGAAACACAGAAATCCAACCTAGAG TyrIleProLysAspGlnLysTyrSerPheLeuHisAspSerGlnThrSerPheCysPhe -----AACCCCCAGACCTCCCTCTGTTTC 255 80

CTGCTCCGCATCTCCCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG SeraspSerIleProThrProSerasnMetGluGluThrGlnGlnLysSerAsnLeuGlu 100 120

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Endocrinology 13) 1744-1782, 1993
AvTitles (Idning of Kour growth homens/chorinoic commencementorpin-related complementar
Avjeterence number: 183857, SUID:94009724; PMID:8404617
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A; Residues: 1-217 < RES>
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             CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCCTATCCAGGCTTTTTGACAACGCTAGT 120
                                                                                                                                                                            TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAACAAAATCCAACCTAGAG 255
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                                                                                                             CTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG 315
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A;Cross-references: UNIPROT:Q07367; GB:L16552; NID:g293108; PIDN:AAA18839.1; PID:g293109 C;Superfamily: prolactin
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Endocrinology 13, 1944-192, 193
Reduction Logy 13, 1944-192, 193
Note ten county of four growth hormone/closicate seminentropin-related complementary
Note ten county of four growth hormone/closicate
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C.Specise: Meacas milatta (thesus macaque)
C.Date: 31-May-1996 Heequence_revision 31-May-1996 Hrext_change 09-Jul-2004
C.hacession: 133267
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US-09-856-796B-1 (1-609) x I53267 (1-217)

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A;Molecule type; mENA
A;Molecule type; mENA
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Bodoczinology 13, 1744-1752, 1993
A.TILER Cloung of Four growth borouse/chorionic sometomamocropin-related complemental
A.FELERMON manufact 153557; MUID-9408773; PMID-8404817
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C.Species: Macaca mulatta (themsu macaque)
C.Date: 31.May-1996 #sequence_revision 31.May-1996 #text_change 09-Jul-2004
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G.Superfamily: prolectin
F:1-26/Domain: sygnal sequence #status predicted <NATY
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A;Molecule type: DNA
A;Residues: 1-215 <HIR>
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C)Accession, 167408 M.F. Febr. J.W.; Pouler, P.D.
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A;Cross-references: UNIPROT:Q07368;
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ACTIGGGGGAARTCCAGCAGCAGTTCGACCAGCAGTGAC
159 ThrOlyGlnTlacLeuLygGlnThrTyrSerLygSheAepThrAsnSerHisAsnHisAsp
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                                                            GlyIleGluThrLeuMetTrpArgLeuGluAspGlyIleProArgThrGlyHisIlePhe
                                                                                                                         GGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGGACTGGGCAGATCTTC
                                                                                                                                                                    AsnLeuLeuHisHisThrSerAspSerAspValHisAspLeuLeuLysAspLeuGluGlu
                                                                                                                                                                                                                                       AGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTAAAGGACCTAGAGGAA 390
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A;Molecule type: DNA
A;Residues: 1-199 <CHE>
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R(Chor. 8.17, 13a, 7.4.; Seeburg, RcChor. 8.17, 13a, 7.4.; Seeburg, Gononice 4. 479-497, 1989
A)Title: The Duman growth bormone locus; nucleotide sequence, biology, and evolution. A)Reference number: A23435; MXID:89307277; PMID:2744760
A)Reference number: A23435; MXID:89307277; PMID:2744760
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C:Spacies: Homo sapiens (man)
C:Date: 29-Dec-1989 #aequence_revision 29-Dec-1989 #text_change 09-Jul-2004
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SerHisAsnHisAspAlaLeuLeuLysAsnTyrGlyLeuLeuHisCysPheArgLysAsp
                                                      GATGGCAGCCCCCGGACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAAAC
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                                                                                                                   AspGlySerHisLeuThrGlyGlnThrLeuLysGlnThrTyrSerLysPheAspThrAsn
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C:Ruperimally: prolacth
C:Ruperimally: prolacth
F:1-26/Domain: signal sequence Hearths predicted «NAT»
F:78-189;206-214/Disulfide bonds: #tothus predicted
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A/TLIE: A dog growth hormone cDNA codes for a mature p
A/TLIE: A dog growth hormone
A/TEGERENE MADET; 446145; MUID:34265166; PMID:3205387
A/TEGERUM DPA:146145; MUID:34265166; PMID:34265187
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WAltermate names; growth bormone
(Japenies: Gania lupum familiaris (dog))
Clades: 19-Dec-1997 Meaquesca previation 19-Dec-1997 Heart_change 09-Jul-2004
(Jacomston: 146125, 38199)
Malactoco-begitings, JAX-B merceta-Galdama, H.A.
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A;Note: submitted to the EMBL Data Library, June 1993
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submitted to the Atlas, May 1971
A;Reference number: A94594
A;Accession: A94594
                                                                                                                                                  A;Accession: A01516
A;Mclecule type: protein
A;Residues: 27-30;149-194,'N',196-216 cMIL>
R;Mills, J.B.
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I. BAGI. Chem. 245, 3407-3415, 1970
AlFilto Cymnogen bromide cleavage and partial am
AlFilto Cymnogen bromide cleavage and partial am
AlFederence number: A03554, WHID-7023161; PMID-44
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A; Residues: 97-108, 'E', 110-158 < YAN>
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ANSAcute type make 108, VY, 20, 21, VG, 73-44 eSDS.
A Group ordermous (08/2013, MIDG)44479; PINK: AA.
CHOMBOOK OF COMMON (18/2013, MIDG)4479; PINK: AA.
CHOMBOOK OF COMMON (18/2013, MIDG)4479; PINK: AA.
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A;Residues: 1-216 cACN;
A;Ccose-references: GB:X53325; NID:g288361; PIDN:CAA37411.1; PID:g288362
R;Seeburg; P.H.; Sias, S.; Adelman, J.P.; de Boer, H.A.; Hayfilck, J.; J
DM, 2, 17-45; 1863
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A; Residues: 1-216 < VIZ>
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CTACTCAAGAACTACGGGCTGCTCTACTGCTT CAGGAAGGACATGGACAAGGTCGAGACA
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TyrLeuArgValMetLysCysArgArgPheValGluSerSerCysAlaPhe TTCCTGCGCATCGTGCAGTGCCGCTCT---GTGGAGGGCAGCTGTGGCTTC

Access-references: UNIFOR:Pol/148; GBHM/744; ND:pj44475; PIDM:AAA1044.]; PD:pj54476; R&RACO, Y.; Shinokawa, N.; Rato, T.; Hirsi, T.; Yoshihama, N.; Rato, T.; Hirsi, T.; Yoshihama, N.; Rato, T.; Hirsi, T.; Yoshihama, N.; Rato, H.; Hatter, M.; Alleries of the State o

J.; Jnurani,

900

A; Title: Efficient bacterial expression of bovine and p A; Reference number: I45898; MUID:83209123; PMID:6303731 bovine and porcine growth hormones

A;Molecule type: mRNA A;Molecule type: mRNA A;Cross-references: GB:M27326; NID:g164477; PIDN:AAA31045.1; PID:g164478

A.Title A multisite-directed mutagenesis using T7 DNA polymerase. A.Reference number: 146885; MUID:89137997; PMID:3224824 A.Accession: 146885 application

PIDN: MAA31046.1; PID: 9164480 porcine growth normone (pGH) gene

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A . B

tial amino acid PMID:4918150 sequence of porcine growth hor

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CiSpecies: Pelie silvestris cotus (domestic cat)
CiDate: 10-3pc-1996 sequence_revision 24-May-1996 stext_change 09-Jul-2004
CiAccession: UC662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (c) Superfamily: prolactin
C; Keywords: anterior pitutary; growth factor; he
F1, -26/Domain: signal sequence Hetatus predicted
F2, -216/Product: somatorropin Hetatus predicted
F7, 78-199/Disulfido bonds: Hetatus predicted
F7, 78-199/Disulfido bonds: Hetatus experimental
F7, 78-199/Disulfido bonds: Hetatus experimental
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A; Residues: 140-148 <MI2>
C; Genetics:
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                                                                                                                                                                     TyrLeuArgValMetLysCysArgArgPheValGluSerSerCysAlaPhe 216
                                                                                                                                                                                          TTCCTGCGCATCGTGCAGTGCCGCTCT---GTGGAGGGCAGCTGTGGGCTTC 606
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C,Superfamily: prolactin
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C,Ecywords: pituitary
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Gene 166, 207-269, Section coding for out proach harmone and prolaction.
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AlExperimental mource: pituitary
C)Commetics
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somatotropin precursor - rabbit

849483 RESULT 믕

15

Job time : 40 secs

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NAIternate names growth hormone
CiSpecies Cryctolgase uniculus (demestic rabbit)
CiDates 20. RSb-1995 #sequence_revision 20-Peb-1995 #text_change '09-Jul-2004
CiAccession 894813 .
R:#ells, O.C.; Wallis, M.
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C;Superfamily: prolactin
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A; Reference number: S49483
A; Accession: S49483
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A; Residues: 1-216 <WAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, October 1994
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200 TyrLeuArgValMetLysCysArgArgPheValGluSerSerCysValPhe 216
                              559 TICCTGCGCATCGTGCAGTGCCGCTCT---GTGGAGGGCAGCTGTGGCCTTC 606
                                                                                                            180 LeuLeuLysAsnTyrGlyLeuLeuSerCysPheLysLysAspLeuHisLysAlaGluThr
                                                                                                                                                      160 GlyGlnLeuLeuLysGlnThrTyrAspLysPheAspThrAsnLeuArgGlyAspAspAla
                                                                                                                                                                                                                                                                                     439 GGGCAGATCTTCANGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGACGCA 498
                                                                                                                                                                                                                                                                                                                                                  140 AspLeuGluGluGlyIleGlnAlaLeuMetArgGluLeuGluAspGlySerProArgVal 159
                                                                                                                                                                                                                                                                                                                                                                                                        379 GACCTAGAGGAAGGCATCCAAACGCTGATGGGGAAGGCTGGAAGATGGCAGCCCCCGGACT 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319 GTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TyrlleProGluGlyGlnArgTyrSerIleGlnAsnAlaGlnAlaAlaPheCysPheSer 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 LeuArgAlaGlnHisLeuHisGlnLeuAlaAlaAspThrTyrLysGluPheGluArgAla 60
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                                                                                                                                                                                                                        Unpublished (1999)
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National Institutes of Health, P
                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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AGENCOURT 13979169 NIH MGC 179 Homo sapiens CDNA clone
TMAGE 130368973 5', mRNA sequence.
                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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CD251386 817 bp mRNA linear EST AGENCOURT_14204245 NIH_MGC_179 Homo sapiens cDNA clone

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High quality sequence stop: 730.
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                                                                      GATGGCAGCCCCCGGACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAAC
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CD251386
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http://image.llnl.gov
plate: NDAM448 row: l column: 17
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Tishum Procurement: Dr. McLand: Brownstein
CDNA Library Preparation: Invitrogen Coop
CDNA Library Arayed by: The I.M.A.G.B. Consortium (LLANL)
DNA Sequencing by: Agencourt Bloncience Corporation
DNA Sequencing by: Agencourt Bloncience Corporation can
close distribution: MC Clone distribution, Information can
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//Limms_type_"Rightsy", and TS phage resistances)*

//Limms_type_"Rightsy type_type_"Rightsy type_"Rightsy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library.
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CTTCAAGAGGGCAGTGCCTTCCCCAACCATTCCCTTATCCAGGCTTTTTTGACAACGCTAGT Similarity

99.2%;

Score 604.2; DB 6; pred. No. 3.3e-147; 0; Mismatches 3;

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                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa; Chordata; Crmiata; Vertebrata; Enteleostomi;
Mammalia, Buthoria; Friantes; Catarrhini; Hominidae; Homo.
L., 1988e 1. C., 270)
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CNN Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNN Sequencing by: Agencourt Bioscience Corporation
DNN Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can
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Matches 602;

Best Local Similarity

Indels

Gaps

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KEYWORDS SOURCE ORGANISM 밁 ġ ą REFERENCE VERSION ACCESSION DEFINITION 10Cus RESULT 7 ORIGIN FEATURES COMMENT AUTHORS TITLE Query Match JOURNAL Bource 633 600 573 541 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999) Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Michael Brownstein Mammalia; Eutheria; 1 (bases 1 to 958) Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. EST CD242555.1 CD242555 CD242555 AGENCOURT_14121225 NIH_MGC_179 Homo Plate: NDAM452 row: 9 Contact: Robert Strausberg, Ph.D. Homo sapiens Homo sapiens (human) IMAGE:30385394 5', mRNA sequence. TGGCTTCTAG TGGCTTCTAG 609 ATGGAACAAGGTCGAGACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTG ATGG-ACAAGGTCGAGACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTG 96.4%; milarity 98.7%; Conservative e: NDAM452 row: g column: 03 quality sequence start: 20 quality sequence stop: 588. constructed by (Invitrogen), Note: this is a NIH_MGC Library." (timmue,type="bituitary"

//lab.bost="Minish" pan A; [1 and T5 phage remistances)*

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//lab.bost="minish" vector, pow.sponts.1; site 1; soc

//lab.bost="minish" vector, pow.sponts.1; site /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" 1. .958 clone="IMAGE:30385394" Location/Qualifiers GI:31003019 642 Score 586.8; DB 6; Pred. No. 1.2e-142; 0; Mismatches 7; mRNA. sapiens cDNA clone linear Length 958 EST 22-MAY-2003 ECORV 572 632 599 and

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
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NHH-MGC http://mgc.nci.nih.gov/.
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/tissue_type="pituitary"
//ab_host="DRIOR-Ton A ( Ti and TS phage resistances)"
//ab_host="DRIOR-Ton A ( Ti and TS phage resistances)"
//ab_host="bright NGC 199"
//ab_host="Organ: brain; Vector: pCNV-SPORT6.1; Site_1: EcoRV
                                                                                                                                                                                      organism="Homo sapiens"
(mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                        clone="IMAGE:30384149"
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COMMENT

Contact: Qinghua Zhang Shanghai Institute of Endocrinology, Rui-Jin Hospital 197 Rui-Jin II Road, Shanghai 200025, P. R. China

I Chases to 733)
Seng H. Peng Y. Gal, Y. Yang, Y. Gao, G. Xiao, H. Mi, X. Li, N. Gang, B. Peng Y. Gao, A. Cao, R. Cheng, Z. Ma, Z. Gang, L. Ma, S. Li, N. Gang, L. Ma, S. Gang, L. Ma, S. Gang, L. Ma, S. Gang, L. Ma, S. Gang, L. Ma, S. Gang, L. Ma, S. Gang, J. Man, Z. Gang, J. Man, Z. Gang, J. Man, Z. Gang, J. Man, Z. Gang, J. Man, J. Gang, J. Man, J. Gang, J. Man, J. Gang, J. Man, J. Gang, J. Man, J. Gang, J. Man, J. Gang, J. Man, J. Gang, J. Man, J. Gang, J. Man, J. Gang, J. Man, J Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE SOURCE KEYWORDS VERSION DEFINITION LOCUS

Homo sapiens

sapiens (numan)

AV751954 AV751954.1

GI:10909802

AV751954 APD Homo sapiens cDNA clone NPDAZA01 5', mRNA sequence.

EST 19-0CT-2000

AUTHORS ORGANISM AV751954

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Best Local Similarity
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Pax: 86-21-64743206
Email: mbshi@ms.stn.sh.c
This clone is available
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CD107947 797 bp mRNA linear ES
AGENCOURT 14016184 NIH MCC 179 Homo sapiens CDNA clone
IMAGE:30365079 5', mRNA sequence.
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/dev_stage="Adult"
/lab_host="SOLR"
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CD107947.1

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451 376 391 316 256 196

ANGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG

435

510 450 390 315 330 255

TACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA

AAGGACCTAGAGGAAGGCATCCAAAGGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGGAACGTCTATGACCTCCTA 375 CIGCICCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG 271

CIGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGGCCGGTGCAGTTCCTCAGG TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACAGAAACTCCAACCTAGAG TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAACCTAGAG 172 151 121

CTCCGCGCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGAAGAAGCC CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT------

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Tissue Procurement: Dr. Michael Brownstein
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Memmalia, Butheria, primates, Catarthini,
1. (bases 1 to 797)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Umpublished (1999)
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//Golone libe Will McC. 190W-SPORTS 1.1 Site 1: 82
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directionally closed (EcoRet its 8: 80:190-df upon
cloning). Morage insert site 1.1 Mb. Library was
constructed by (Invitrogen). Abotes that 3: 8 MM_MCC
Library."
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/lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
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/mol_type="mRNA"

/db_xref="taxon:9606"
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Catarrhini; Hominidae; Homo.
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Y Match 90.4%; Local Similarity 92.8%; 91 61 31 . CTTCAAGAGGGCAGTGCCTTCCCCAACCATTCCCCTTATCCAGGCTTTTTGACAACGCTATG CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTTGACAACGCTAGT Conservative 0 Score 550.8; DB 6; Pred. No. 3.2e-133; 0; Mismatches 2; Length Indels 45; Site_1: EcoRV Gaps 150 120 90 6

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High quality sequence stop: 765.
Location/Qualifiers
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DDNA Library Arrayed by: The I.M.A.G.E. Consertium (LLML)
BNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MC Clone distribution information can
found through the I.M.A.G.E. Consortium/LLML at:
http://mags.llhl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bages 1 to 798)
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                                                 CTCCGCCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGAAGAAGCC 210
                                                                                                       CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT-----
                                                                                                                                                        CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTATG 150
                                                                                                                                                                                         CTTCAAGAGGGAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT 120
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/db_xref="taxon:9606"
/clone="IMAGE:30367958"
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Pred. No. 3.2e-133;
0: Mismatches 2;
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High quality sequence stop: 634.
Location/Qualifiers
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MA. Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC Clone distribution information can
tround firmsph the I.M.A.G.S. Commortium/LiMI at:
http://msgp:lihi.gov
                                                                                                                                                                                                                                                                                                                       Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                       National Cancer Institute / NIH
                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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AGENCOURT 14214052 NIH MGC_179 Homo sapiens
INAGE:30383909 5', mRNA sequence.
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ORIGIN

Matches

cgapbs-remail.nih.gov

RESULT 13 CD108743 AUTHORS TITLE JOURNAL COMMENT SOURCE ORGANISM DEFINITION REFERENCE Query Match Local Similarity 121 100 376 400 316 340 256 280 196 220 160 640 580 496 520 460 61 607; 556 ÷ CD108743 CD108743.1 CD108743 801 bp mRNA
AGENCOURT 13980109 NIH MGC 179 Homo sapiens
IMAGE 30368844 5', mRNA sequence. NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Unpublished (1999) Bukaryota; Metazoa; Chordata; Mammalia; Butheria; Primates; 1 (bases 1 to 801) Homo sapiens TATATCCCAAAGGAACAGAMGTATTCATTCCTGCAGAACCCCCAGACCTCCCTCTGTTTC CTCCGCGCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGAAGAAGCC CTCCGCCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT------CTTCAMGAGGGAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTATG CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAAGGCTAGT ATGGCTACAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCCTGC AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA AGTGTCTTCGCCAACAGCCTGGTGTACGGGGGCCTCTGACAGGAACGTCTATGACCTCCTA 379 CTGCTCCGCATCTCCTGCTGCTCCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG CTGCTCCGCATCTCCCTGCTGCTCATCCAGTGGCTGGAGCCCGTGCAGTTCCTCAGG TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAMACACAACAGAMATCCAACCTAGAG TCAGAGTCTATTCCGACACCCTCCAACAGGGGGGGGAACACACAGAACAGAAACACCTAGAG ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG 609 GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAAGGACATGGACAAGGTCGAG ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAAGGATGAC ACTGGGCAGATCTTCANGCAGACCTACAGCAAGTTCGACACAAACTCACAAACGATGAC AAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG Conservative sapiens (human) (destroyed); Site_2: Not1; Library is oligo-dT primed directionally cloned (ScoRV site is destroyed,upon cloning). Average insert site it. b. bibbary was constructed by (Invitrogen). Note: this is a NHH_MGC Library 90.41; GI:30761917 Score 550.8; DB 6; Pred. No. 3.2e-133; 0; Mismatches 2; Craniata; Vertebrata; Catarrhini; Hominidae; AACCCCCAGACCTCCCTCTGTTTC Gene Indels Length linear cDNA clone Collection 45; Euteleostomi EST 15-MAY-2003 693 (MGC and 315 339 255 279 219 171 99 60 555 579 495 519 439 459 399 639 Ş 8 Ş 밁 Ş 밁 S 무 Ś 몽 S 문 Q 뭉 Ş 문 망 S ₽ S

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KEYWORDS VERSION

Contact: Robert Strausberg, Ph.D

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556 581 496 521 436 461 376 401 341

GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAAGGACATGGACAAGGTTCGAG ACTOGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAACGATGAC ACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACACAAACGATGAC ANGGACCTAGAGGANGGCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGG ANGGACCTAGAGGANGGCATCCAAACGCTGATGGGGAAGGCTGGAAGATTGGCAGCCCCCGG AGTGTCTTCGCCAACAGCCTGGTGTACGGCGGCTCTGACAGCAACGTCTATGACCTCCTA AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA

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۳.	SOMA HUMAN STANDARD; PRT; 217 AA.
'n	P01241; Q14405; Q16631; Q9HBZ1; Q9UMU7; Q9UNL5;
Ä	21-JUL-1986 (Rel. 01, Created)
Ä	01-MAR-1992 (Rel. 21, Last sequence update)
Ä	25-OCT-2004 (Rel. 45, Last annotation update)
Ħ	Somatotropin precursor (Growth hormone) (GH) (GH-N) (Figureary Growth
×	hormone) (Growth hormone 1).
쭏	Name=GH1;
ĕ	Homo sapiens (Human).
ñ	Bukaryota; Metazoa; Chordata; Craniata; Vercebraca; Bucerount;
ñ	Mammalia; Eutheria; Primates; Catarrini; nominicae; nomo.
×	NCBI_TaxID=9606;
ž	(E)
Ŧ	SEQUENCE FROM N.A. (ISOFORM 1).
×	MEDLINE=80034477; PubMed=386281;
S	Roskam W., Rougeon F.;
ã	"Molecular cloning and nucleotide sequence of the number o
7	structural gene.";
e	Nucleic Acids Res. 7:305-320(1979).

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MEDLINE=72143935; PubMed=5144027;
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L1 C.H., Dixon J.S., Liu W.-K.;
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MEDIALE-8613739; behaved-3912261; DOI:10.1016/0378-1119(85)90319-1;
MEDIALE-8613739; behaved-3912261; DOI:10.1016/0378-1119(85)90319-1;
Periplanel production of correctly processed human growth homome
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"A novel gone expressed in human pituitary.";
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Chen E.Y., Liao Y.C., Smith D.H.,
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DNA 1:239-249(1982).
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LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg CTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGG TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAACCTAGAG LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPheGluGluAla CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT------LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnValMet CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTAGT MetalaThrGlySerArgThrSerLeuLeuLeuAlaPheGlyLeuLeuCysLeuProTrp

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InterPro; IR001400; Scamatotropin.
Ffam; PF00103; Normone j. 1
Ffam; PF00103; Normone j. 1
Ffam; PF00103; SCMATÖTRODIN.
ROLLERS; PR00836; SCMATÖTRODIN.
                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-2004) to the EMBL; AY613431; AAT11508.1; HSSP; P01241; 1A22.
                                                                                                                                                                                                                                                                                                                                                                                                                   Jorge A.A.L., Arnhold I.J.P.,
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Mammalia; Eutheria; Primațes; Catarrhini; Hominidae; Homo.
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28-FEB-2003 (Rel. 41, Last sequence update)
05-UUL-2004 (Rel. 44, Last amnotation update)
Somatotropin precursor (Growth hormone) (GH)
hormone) (Growth hormone 1).
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PROSITE; PS00266; SOMATOTROPIN_1; 1.
PROSITE; PS00338; SOMATOTROPIN_2; 1.
SEQUENCE 217 AA; 24946 MW; 72D079DES2BDB51A CRC64;
                                                                                                                                                             PRINTS; PRO0836; SOMATOTROPIN.
                                                                                                                                                                                                       GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005179; F:hormone activity; IEA.
InterPro; IER009079; 4 helix_cytokine.
InterPro; IER001400; Scmatotropin.
                                                                                                                                                                                                                                                                                               Homo smylens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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05-JUL-2004 (TrEMBLrel. 27,
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01-OCT-1993
01-OCT-1994
MEDIJES-9408972; PubMed-9404677; DOI=10.1210/en.133.4.1744; Golos T.G., During M., Fisher J.M., Fouder P.D.; Coloning of four growth hormone/operionic sometensemetropin-related complementary decrythouselast actual differentially expressed during pregnancy in the rhesis monkey placenta.";
                                                                                                                                                                                  Bukaryota, Matazoa, Chordata, Craniata, Vertebrata, Enteleostomi, Mammalia, Euteneria, Primates, Catarrhini, Cercopithecidae, Corcopithecidae, Mecaca.
                                                                                                                                                                                                                                                                                            Oi-OGT-1993 (Rel. 27, Created)
O1-OGT-1994 (Rel. 30, Last sequence update)
O5-UHL-2004 (Rel. 44, Last sequence update)
Sematocropin procussor (Growth hormone) (GH)
hormone) (Growth hormone 1)
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                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                          SOMA_MACMU
                                                                                                                                                                    TaxID=9544;
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-I- SIMILARITY: SUBCELLULAR LOCATION: Secreted Belongs to the somatotropin/prolactin family

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBN outeration of the Burgean Bioinformatics Institute, There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this sequement is not removed. Usage by and for commercial. entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). EMBL; L16556; AAA18842.1; -.

DISULFID DISULFID CONFLICT CONFLICT Direct PROSITE; PS00266; SOMATOTROPIN_1;
PROSITE; PS00338; SOMATOTROPIN_2; PRINTS; PRO0836; SOMATOTROPIN. Pfam, PF00103; Hormone_1; InterPro; IPR009079; 4 helix cytokine InterPro; IPR001400; Somatotropin. HSSP; P01241; 1AXI procein sequencing; Hormone; 179 Somatotropin.
By similarity.
By similarity.
E -> Q (in Ref.
N -> D (in Ref. -> Q (in Ref. 2) -> D (in Ref. 2) 2C5180341EEC46D0 Pituitary; Signal

Percent Similarity: Scores: Similarity: 2.6e-76 981.50 90.32* 88.94* 88.26* Length: Matches: Conservative: Mismatches: Indels: 217 193

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61	μ	,
61 CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTTGACAACGCTAGT 12	1 MetAlaAlaGlySerArgThrSerLeuLeuLeuAlaPheAlaLeuLeuCysLeuProTrp 20	1 ATGGCTACAGGCTCCCGGACGTCCCTGCCTCTGCCTCTGCCTCTGCCTGC
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LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnAlaMet

40

196 81 TCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAACCTAGAG TyrIleProLysGluGlnLysTyrSerPheLeuGlnAsnProGlnThrSerLeuCysPhe lnLysSerAsnLeuGlu

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placental growth hormone 20kDa imoform precursor.
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MEDLINE-98373737, PubMed-9709963; DOI=10.1210/jc.83.8.2878;
Boguszewski C.L., Svensson P.A., Jansson T., Clark R.,
Carlsson L.M.S., Carlsson B.;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Growth hormone variant precursor (GH-V) (Plac
This $MISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation the Buropean Bioinformatics Institute. These are no restrictions on its
                                                                                                                                                     Revol M. sequivel D. santiago D. Barroan-shidama H. Anthropoldean lineages ', mentago event horozone gene in three Anthropoldean lineages ', mentago event horozone gene in the Shemited (MPS 1201) To the mentago event in great potential to shemited (MPS 1201) To the mentago event in the control its major - tols in standisting body growth is to stimulate the lines and other tissease to secrete 167: It stimulates both the differentiation and polification of myoblasts. It also stimulates mainto said supeks and protein graythess in meals and other assets.

    -!- TISSUE SPECIFICITY: Expressed in the placenta.
    -!- SIMILARITY: Belongs to the sometotropin/prolactin family.

                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hormone) (Growth hormone 2)
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                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=GH2
                                                                                                                      SUBCELLULAR LOCATION: Secreted.
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Catarrhini; Hominidae, Pan.
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PROSETTE; BEGGO388; SOMATOTROPIN 2; 1.
PROSETTE; PROGEOR; Placenta; Signal.
Glycoproteil; Hormone; Placenta; Signal.
GRAIN 2; 2; Growth hormone
CHAIN 27 217 Growth hormone
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PRINTS; PR00836; SOMATOTROPIN
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PRINTS, PRO0835; SONATOTROPIN,
PROSITE; PRO0356; SONATOTROPIN 1; 1.
PROSITE; PS00356; SONATOTROPIN 2; 1.
PROSITE; PS00356; SONATOTROPIN 2; 1.
SEQUENCE 217 AA; 25001 M#; P24CO5312EB37988
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Mammalia; Eutheria;
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Mammalka; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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.C., Smith D.H., Barrera-Saldana H.A., Gelinas R.B.,
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EMBL; K00470; AAA598619.1; EMBL; J03756; AAB59548.1; EMBL; J03756; AAB59548.1; EMBL; J03751; AAA55891.1; EMBL; J03071; AAA55852.1; EMBL; J03071; AAA5552.1; EMBL; BC020760; AAH20760.1;

HSSP, P01241, 1A22. PIR; A28072; STHUV2 PIR; D32435; STHUV.

STHUVZ.

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Alternative splicing, Glycoprotein, Hormone, Placenta, Polymorphism,

PROSITE; PS00266; SOMATOTROPIN 1; 1.
PROSITE; PS00338; SOMATOTROPIN 2; 1 PRINTS; PRO0836; SOMATOTROPIN. InterPro; IPR009079; 4 helix cyto) InterPro; IPR001400; Somatotropin. GO; GO:0005179; F:hormone activity; Ty InterPro; IPR009079; 4_helix_cytokine. H-InvDB; HIX0014077; -. Genew; HGNC:4262; GH2

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or send an email to license@isb-sib.ch).
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Betroeffield Y.S.M., Terywintek III., Schläde U., Smillum D.E.,
Schmerch A., Schlein J.E., Jones S.J.M., Merze N.A.,
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memoration and Mitchial analysis of more than 15,000 full-length human
from Natl. Acad. Sci. U.S.A., 9916899-16901(2002).
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Name-1, Synonyma-64-ini
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Name-2, Synonyma-64-ini
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Hoolde0124-2; Sequence-185 066201;
TISSUM selection of the Name Jalenta.
SPHIANTIFI. Models to the name topy-in/polacetin family.
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FINCTION: Playe an important role in growth control. Its major role in stimulating body growth is to etimulate the liver and other timume to secrete 18-1. It etimulates both the differentiation and protlibration of spoblames. It also etimulates antino scid uptake and protein symbolates. It also etimulates amino scid uptake and protein symbolates.
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databa
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US-09-856-796B-1 (1-609) x SOMA_SAIBB (1-217)

Query Match: Pred. No.: Best Local Similarity: Percent Similarity: Score:

1.2e-69 904.50 86.64* 82.03* 81.34*

Mismatches: Indels: Matches: Conservative: SEQUENCE DISULPID DISULFID

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Bukaryota Metazoa (Chordata; Craniata; Versbartar Burkostomi)
Mammalia, Butheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
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(Rel. 44, Last annotation update)
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Callithix jacchus (Common marmoset.
Bukayyota Metacoa; (Cordata; Crantata; Vertebrata; Butaleostomi
Mammalia; Butheria; Primates; Platyrrhini; Callitrichidae; Callit
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      This SWISS-PROT entry is copyright; It is produced through a collaboration between the Swiss neutron setting. There are no restrictions on its use of the Swiss neutron setting. There are no restrictions on its use by non-positi institutions along as its concern is in no way non-positi institutions along as its concern is in no way endicing and this statement is not removed. Usage by and for commercial entities required as ilcomes agreement (see http://www.libeship.ord.neutron.com
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05-JUL-2004 (Rel. 44, Last annotation update)
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PROSITE; PS00266; SOMATOTROPIN 1;
PROSITE; PS00338; SOMATOTROPIN_2;
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InterPro; IPR001400; Somatotropin.
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ACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC
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PRINTS; PR00836; SOMATOTROPIN.
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J. Clin. Endocrinol. Metab. 83:2878-2885(1998)
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MEDLINE-98137377, PubMed-9709963; DOI=10.1210/3c.83.8.2878;
BOGURZEWSKI C.L., Svenseon P.A., Jansson T., Clark R.,
Carlsson L.M.S., Carlsson B.;
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Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
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GO; GO:0005179; F:hormone activity; IEA.
InterPro; IRR003979; 4 halix cytokine.
InterPro; IRR001400; Somatotropin.
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                                                                         SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrArgHisLeu
                                                                                                                              AGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTATGACCTCCTA
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Catarrhini; Hominidae; Homo.
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hGH-V3 precursor.
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leuGlnAlaHisArgAlaTyrGlnLeuAlaIleAspThrTyrGlnGluPheGluGluAla 60 CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTT-----LeuGlnGluAlaGlyAlaValGlnThrValProLeuSerArgLeuPheAspHisAlaMet 40 CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGGTAGT 120 MetAlaAlaGlySerArgThrSerLeuLeuLeuAlaPheAlaLeuLeuCysLeuProTrp

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US-09-856-796B-1 (1-609) x Q866U1 (1-217)
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HSSP, 70.141, L.22.

GJ 60.005576; Grextmodillar; IBA.

GJ 60.005579; Formome activity; IBA.

ING 60.005179; Formome activity; IBA.

ING 60.005179; Formome activity; IBA.

ING 60.00570; Formome activity; IBA.

ING 60.00570; Formome activity; IBA.

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"The GH-PL locus a hot-point between human and chimpanzee
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Expansion and divergence of the GH locus between spider monkey and chimpanzee."
Gene 336:185-193(2004).
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PubMed-1524630, DO:=10.1016/j.gene.2004.03.034;
PubMed-1524630, DO:=10.1016/j.gene.2004.03.034;
Revol De Mendoza A., Bequivel Escobedo D., Martinez Davila I.,
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Pan troglodytes (Chimpenzoe).
Bukaryota Metazoa; Chordata; Craniata; Vertebrata;
Bukaryota Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Primates; Catarrhin; Hominidae;
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